

FIG. 1A

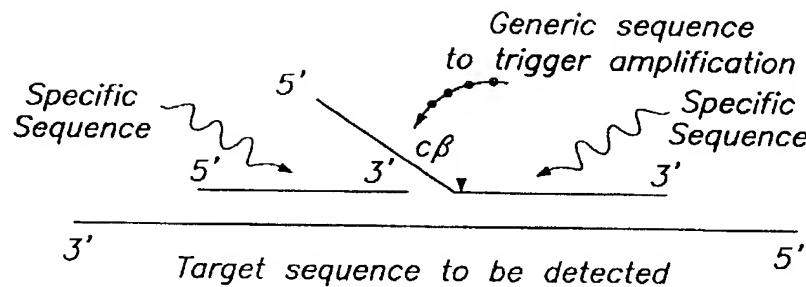


FIG. 1B PART ONE: TRIGGER REACTION

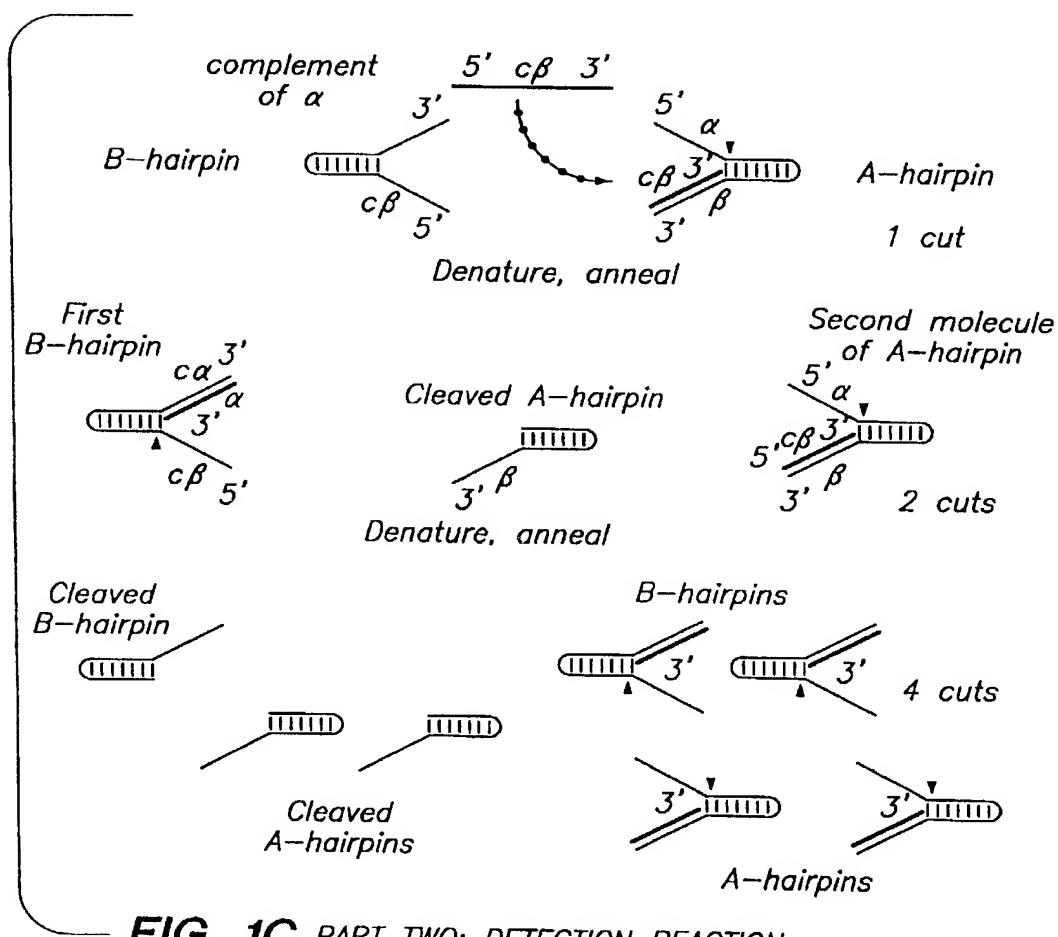


FIG. 1C PART TWO: DETECTION REACTION

FIG. 2A

FIG. 2B

MAJORITY AGGGCCACGGGACCTTACCAAGCTTCCGACCCATCGGCGCTCCACGGGAGGGAACTCA

DNAPTAQ	AAA	T	CA	487
DNAPTFL	T	G	A	484
DNAPTR	A	G.C.	T	490
		G	CC	

MAJORITY T C A C C C G G G G T G G C C T T T G G C A G A A G T T A C G C C T G A G G C G A C T T G G A C T T A C C G G C C T G G C

DNAPTAQ	C.	A.	A.	557
DNAPTF1	A.	C.	C.	554
DNAPTM	A.	C.	C.	560

MAPTAA	E.....GAG.....T.....	G.....GAG.....T.....GG..	627
MAPTFL	G..1.....A.....6.	A.....G.....A.....GGC..	624
MAPTTR		TC.....A.....A.....A..	630

APTAU	G.	C.	C.	A.	A.	694
APPFEL	T	C.	C.	A.	T.	691
APTR	A.	A.	A.	A.	A.	700

FIG. 2C

DNAPTAO	[SEQ ID NO:1]	...T.....	C.....T.....A.....	C.....GG.....A.....	764
DNAPTFL	[SEQ ID NO:2]	...GGG.....	G.....C.....GGG.....T.....	C.....A.....T.....	761
DNKAPTR	[SEQ ID NO:3]	...A.....	C.....A.....C.....G.....T.....	C.....G.....C.....G.....	770

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ADDITIONAL INFORMATION

FIG. 2D

MAJORITY [SSEQ ID NO:7]	CGGGGXCCTCCCTCCCCAAGGAGCTGGCCCTTGGCCCTAGGGAGGGCCTXGACCTCTGGGGGGAGG	1114
DNAPTAQ [SSEQ ID NO:11]G.....T.....A.....AG.....C.....A.....T.....G.....CC.....C.....	1114
DNAPTFL [SSEQ ID NO:2]AA.....G.....G.....C.....G.....T.....G.....A.....A.....	1111
DNAPTRH [SSEQ ID NO:3]C.....G.....C.....C.....TC.....G.....A.....G.....	1120
MAJORITY	ACCCATGGCTCCGGCTAACCTGGACCCCTCCAAACACCAACCCCCAGGGGCTGGGGGGCTAACGG	1184
DNAPTAQG.....T.....G.....T.....T.....T.....T.....	1181
DNAPTFLG.....T.....G.....T.....T.....T.....T.....	1190
DNAPTRHG.....T.....G.....T.....T.....T.....T.....	1180
MAJORITY	GGGGAGTGGACGGAGAXGGGGGGAGGGGGCTCCCTGGAGAGGCTCTCCXGAACCTXXXGGAG	1254
DNAPTAQ	C.....G.....T.....A.....GG.....C.....C.....A.....G.....	1251
DNAPTFLT.....A.....GG.....C.....C.....G.....AAT.....	1260
DNAPTRHC.....C.....GG.....C.....G.....CAT.....G.....	1260
MAJORITY	GGCCTTGGGGAGGAGGGCTCCCTGGCTTACGAGGAGTGGAGAAGCCCTTCCGGTCCCTGG	1324
DNAPTAQ	A.....G.....A.....A.....AC.....C.....G.....G.....G.....	1321
DNAPTFLA.....A.....AC.....C.....G.....G.....G.....G.....	1330
DNAPTRHC.....A.....C.....C.....A.....A.....G.....	1394
MAJORITY	GGCACATGGAGGGCAGGGGTXGGGCTGGAGCTGGCCCTACCTGGGGGGCTXGACCTGGGGGGAGG	1394
DNAPTAQG.....G.....G.....T.....AG.....T.....G.....G.....	1391
DNAPTFLG.....G.....G.....T.....AG.....T.....G.....G.....	1400
DNAPTRHG.....A.....G.....T.....T.....T.....T.....	1400

FIG. 2E

MAJORITY [SEQ ID NO:71]	GGAGATCCCCCTGGAGGGCTTCCCCACCCCTAACCTAACTGGGGAC	
DNAPIAQ [SEQ ID NO:1]GC.....GC.....	1464
DNAPITL [SEQ ID NO:2]G.G....AG.G.....	1461
DNAPITR [SEQ ID NO:3]T.....G.....	1470
MAJORITY	CAGCTGGAAAGGGCTCTTGGACCTXGGGCTTCCCCCATGGCAAAGACGGAAAGACXGGCAAGC	
DNAPIAQG.....A.....	1534
DNAPITLGC.....G.C.G.T.....	1531
DNAPITRTA.....T.G.G.....	1540
MAJORITY	GCTGGAGGCCCCCTGGAGGGCTXGGXGAGGGCACCCCATGGAGAGATCCCTGGAGTA	
DNAPIAQC.....C.....	1604
DNAPITLT.....G.A.....	1601
DNAPITRG.....A.G.....	1610
MAJORITY	CGGGAGGTGACCAAGCTGAGAACACCTACATXGACCCCTGGGXXCTGGTCCACCCAGGGGG	
DNAPIAQG.....T.....G.A.....	1674
DNAPITLA.....C.C.G.....	1671
DNAPITRG.G.....G.AAG.....	1680
MAJORITY	CGGCTCGCACCCCCCTAACCAAGACGGCACGGGAGGGCTAGCTGGGACCCAACTGG	
DNAPIAQA.....T.....C.....	1744
DNAPITLC.....T.G.C.....	1741
DNAPITRG.....G.....	1750

FIG. 2F

FIG. 2G

MAJORITY	[SEQ ID NO:7]	ACCTTCCCAAGCTGGATTGAGAACCCGGAGGGAGGGAGGGGGTACGGGGAGA	
DNAPTAQ	[SEQ ID NO:1]	2164
DNAPTFL	[SEQ ID NO:2]A.....	2161
DNAPTR	[SEQ ID NO:3]A.....A.....	2170
MAJORITY		CCCTCTTCCGCCGCTACGTGCCGACCTCACGCCCGGCTGAGAGCCGGGGGGA	
DNAPTAQ	C.....A.....AG.G.....	2234
DNAPTFL	T.....	2231
DNAPTR	AA.AA.....	2240
MAJORITY		GGCCATGGCTTACACATGCCGTCAGGCACGCCACCTCATGAACTGGGCACTGGTAAAGCTC	
DNAPTAQ		2304
DNAPTFL	G.....	2301
DNAPTR		2310
MAJORITY		TTCCCCGGCTXAGGAAATGGGGCAGGATGCTCTXAGGTCCACGAGCTGGCTGGGGCC	
DNAPTAQ	A.....GG.....	2374
DNAPTFL	T.....G.....	2371
DNAPTR	C.C.G.....G.....C.....	2380
MAJORITY		CCAAGAGGGGGGAGGGCTGGCCCAAGGAGGTATGGAGGGCTATGCCCTGGGGCT	
DNAPTAQ	A.....A.....CC.....GGCG.....	2444
DNAPTFL	G.....G.....AG.....A.....	2441
DNAPTR	C.....C.....A.....G.....	2450

FIG. 2H

MAJORITY [SEQ ID NO: 7] GCCCCCTGGAGGTGGGATGGGAGGACTGGCTGGCCAGGGACTGAGTAC

DNAPTA0 [SEQ ID NO:1]

DNAPTF1 [SEQ ID NO:2]

DNAPTH [SEQ ID NO:3]

GA

A

CC

GT

FIG. 3A

MAJORITY [SEQ ID NO:8] MXAMMPLFEPKGRVLLVQGHHLAYRTFFALKLITTSRGEPUAVYGFAKSLLKALKEDG- DAVXVVFDAK

TAQ PRO	[SEQ ID NO:4]	. RG.....	H.....	69
TFL PRO	[SEQ ID NO:5]	V.....	V.....	68
TTR PRO	[SEQ ID NO:6]	E.....	YK.....	F.....	70

MAJORITY APSFRHEAYEAYKAGRAPTPEDPROLALIKELVQDGLXRLEVPGYEADDVQLATLAKKAEGEYEVRL

TAQ PRO	GG.....	A.....	139
TFL PRO	V.....	R.....	138
TTR PRO	FT.....	140

MAJORITY TADRDLYQLLSDRIAVLHPEGYLITPAWLWEKYGLRPEQHVDYRALXGDPSSDNLPGVKGIGEKTTAXKLX

TAQ PRO	K.....	H.....	D.....	A.....	T.....	E.....	R.....	E.....	209
TFL PRO	E.....	I.....	Y.....	A.....	I.....	QR.....	IR.....	208
TTR PRO	V.....	V.....	H.....	E.....	F.....	V.....	L.....	K.....	210

MAJORITY EWGSLENLKNLDKVKP-XXREKIXAHMEDIXLISXXLSXVRLDPLPEUDAXRREPDRGSLRAFLERLEF

TAQ PRO	A.....	L.....	AI.....	D.....	K.....	WD.....	AK.....	K.....	R.....	278		
TFL PRO	FOH.....	Q.....	SL.....	LO.....	G.....	AA.....	RK.....	Q.....	H.....	GR.....	T.....	HL.....	277
TTR PRO	ENV.....	K.....	L.....	R.....	LE.....	R.....	L.....	QG.....	280

MAJORITY GSLLHEFGLEXPKALEFAPWPPPECAFUGFULSRREPMMWAELLALAAARRGRUHRAXDPIXGLRDILKEY

TAQ PRO	S.....	K.....	D.....	G.....	PE.....	YKA.....	A.....	348		
TFL PRO	G.....	A.....	SF.....	G.....	WF.....	L.....	Q.....	R.....	G.....	347
TTR PRO	AP.....	K.....	C.....	A.....	A.....	K.....	350

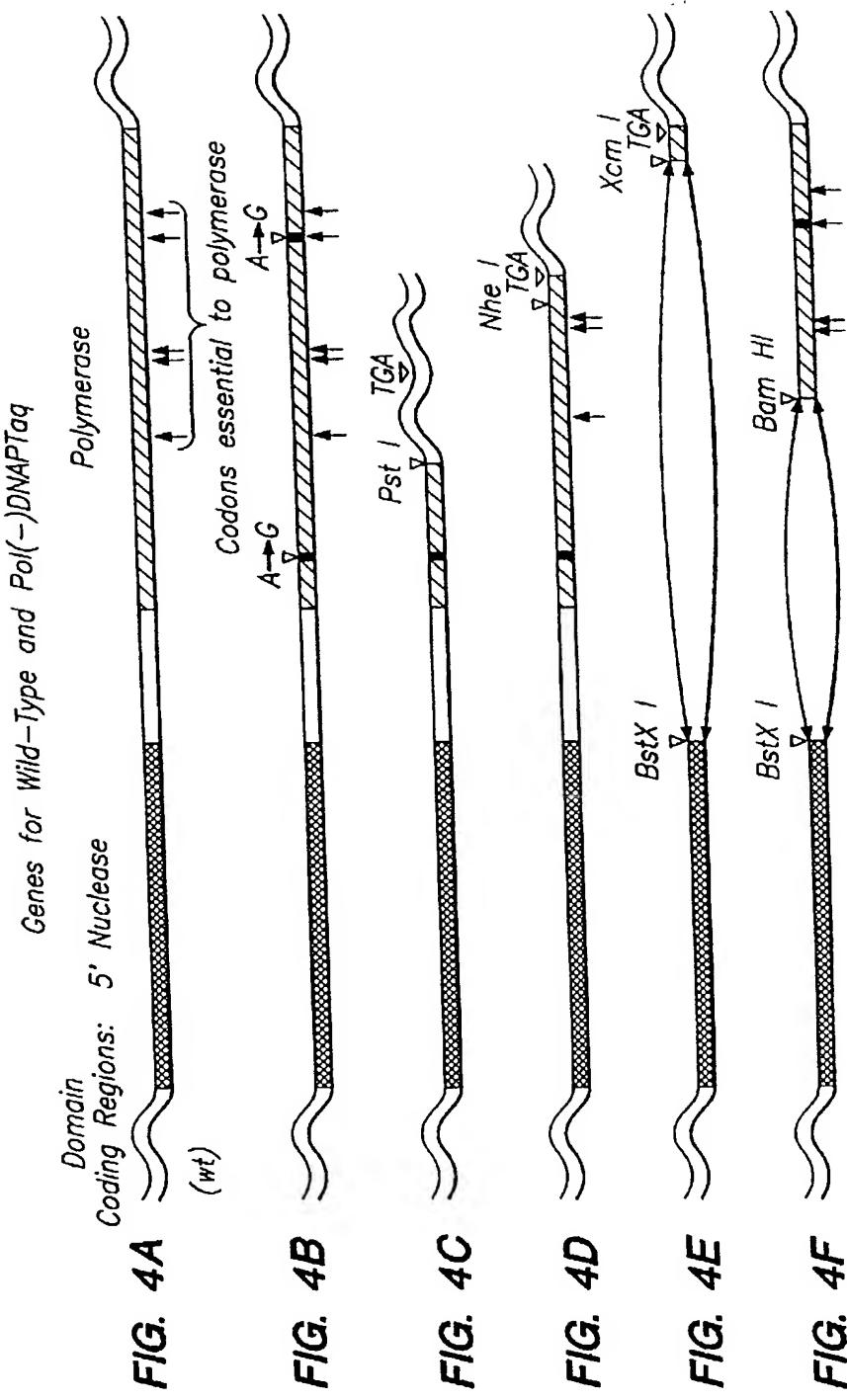
FIG. 3B

MAJORITY [SEQ ID NO:8] RGLLAQDIALVALREFGIDIXPGDDPMILAYLLDPSNITPEGUARRYGGENTEADAGERALLSERLIXXNLXX	
TAQ PRO	[SEQ ID NO:4] S.....S.....G. P.....E.....A.....A.....A.....WG 418
TFL PRO	[SEQ ID NO:5]].....F. E.....A.....A.....Q1. KE 417
TTR PRO	[SEQ ID NO:6] S.....V.....AH.....HR. LK 420
MAJORITY	RLGEFERRLLWLYXFEVKPLSRVLAHMEATGURLDVAYIQLALSLEVAAEIRRLFEEUVFRLAGHPFNLNSRD
TAQ PROR...R...A.....R.....A.....A.....A.....488
TFL PROK.....E.....R.....EA. V. O.....487
TTR PROK.....H.....L.....S.....490
MAJORITY	QLEAVLFDELGLPAGKTEKTKRSTSAAAVLEALREAHPIVEKILQDYLRELTIKLKNTYIDPLPXIUVHPRTG
TAQ PROS.....S.....D. I.....S58
TFL PRODR.....A.....K.....S57
TTR PROH.....V.....S.....S60
MAJORITY	RLHTRFRNOTATATGRLSSSDPHLQNIPURPIQORIRRRAFVAEGWXLVALDYSQIELRVLAHLSGDENL
TAQ PROI.....L.....628
TFL PROV.....V.....627
TTR PROA.....A.....630
MAJORITY	IRUVFQEGRDITHQTASWMFGVPPPEAVDPLMRRAAKTINFQVLYGMSAHRISQELAI PYEEAVAFI ERYFO
TAQ PROE.....R.....Q.....698
TFL PROS. G.....C. S.....697
TTR PROK.....V.....700

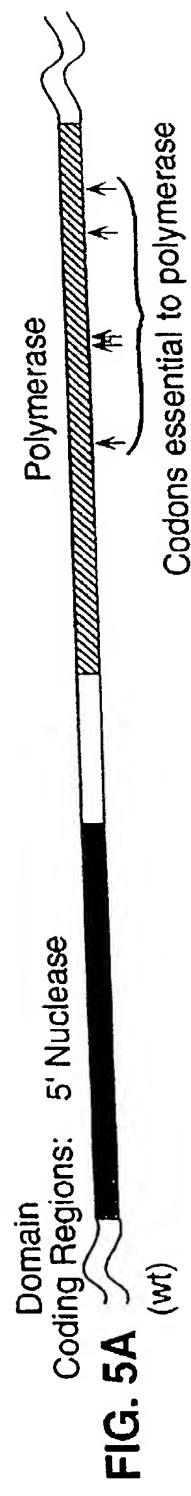
FIG. 3C

MAJORITY [SEQ ID NO:8] SFPKURAWIEKITLEEGRARRCYVETI FGRRRYVUPDINARVKSVERAERMAFNNHPVUGTAADLMKLAUVKL
TAQ PRO [SEQ ID NO:4] E..... 768
TFL PRO [SEQ ID NO:5] .Y..... G..... R. 767
TTH PRO [SEQ ID NO:6] K..... 770

MAJORITY FPRIXEMGARMILQVHDELVLEAPKXRAEXVAALAKEVMEGVYPLAVPLEVVGXGEDWLSAKEK
TAQ PRO E..... E..... A. R..... 833
TFL PRO Q. L..... D..... R..... W. Q..... 831
TTH PRO R. Q. L..... E..... A. KA..... M..... G 835



Genes for Wild-Type and Pol(-) DNAPT1



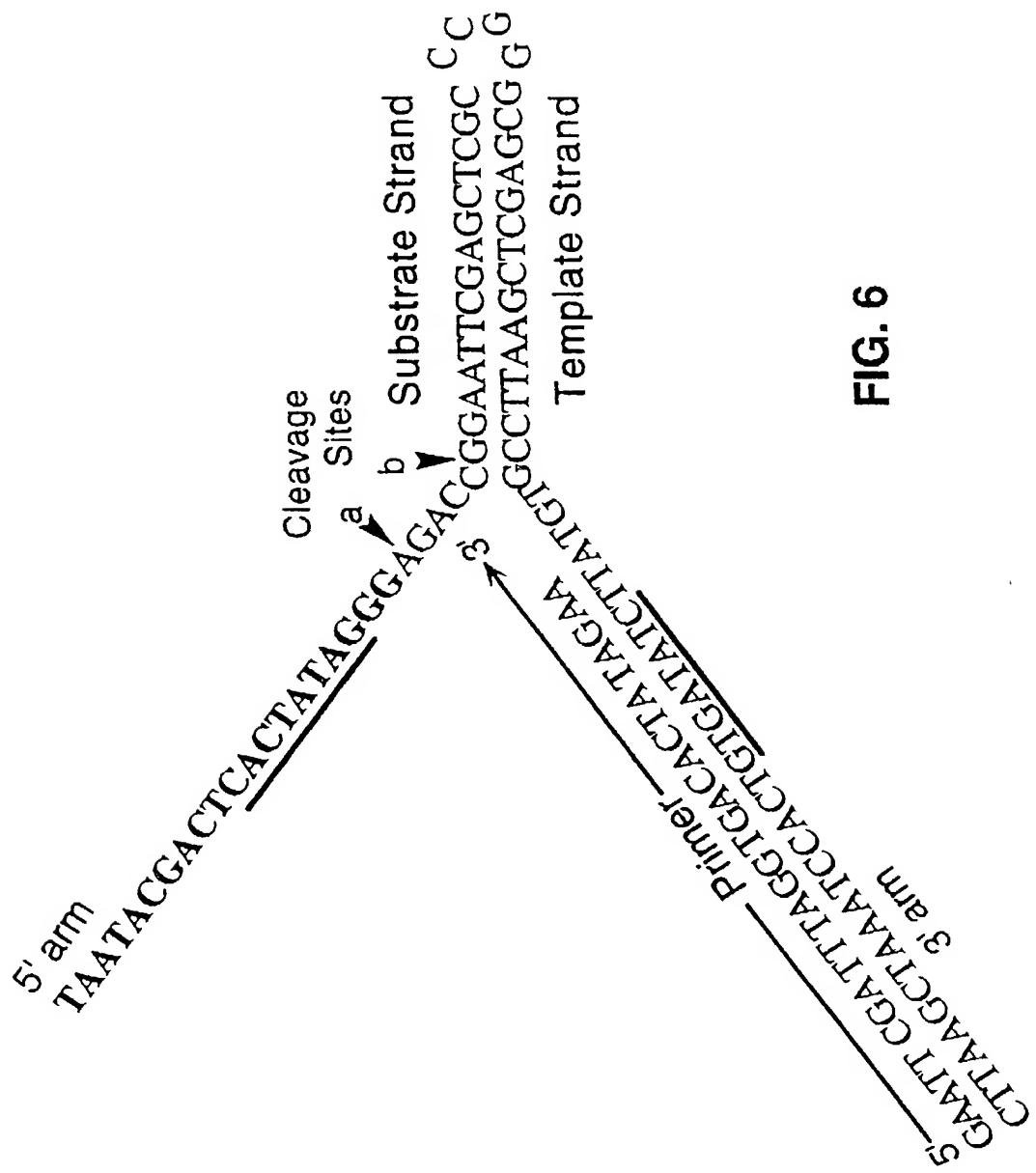


FIG. 6

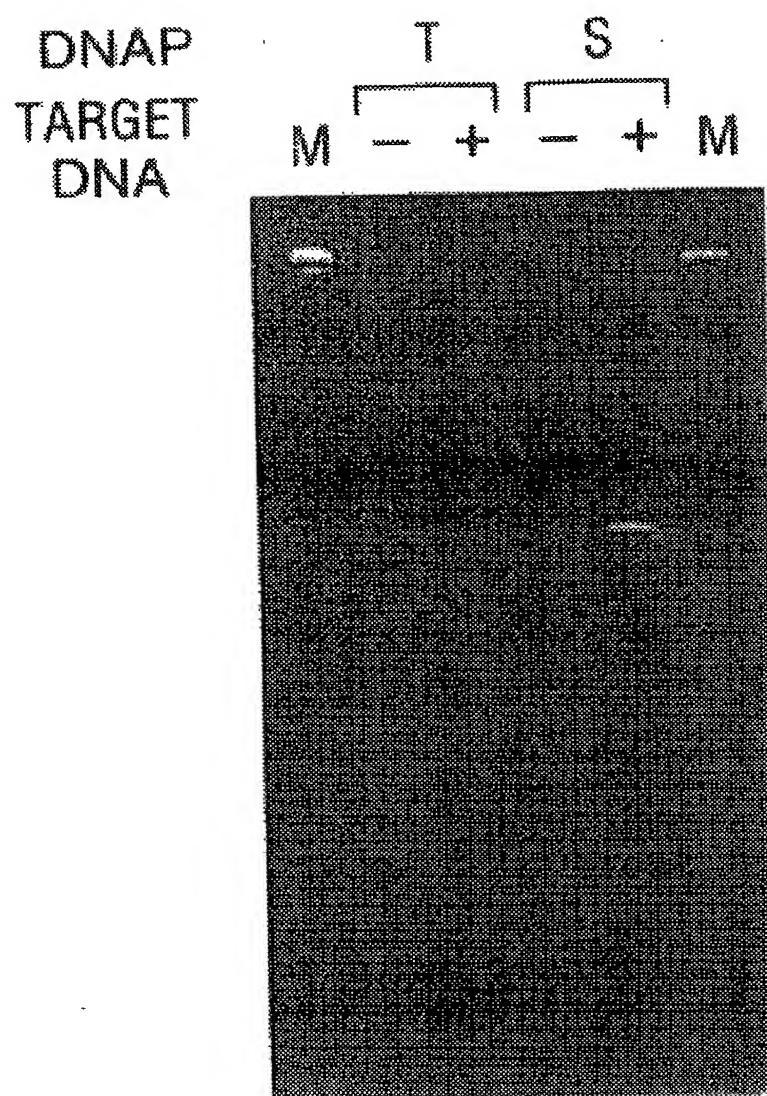


FIG. 7

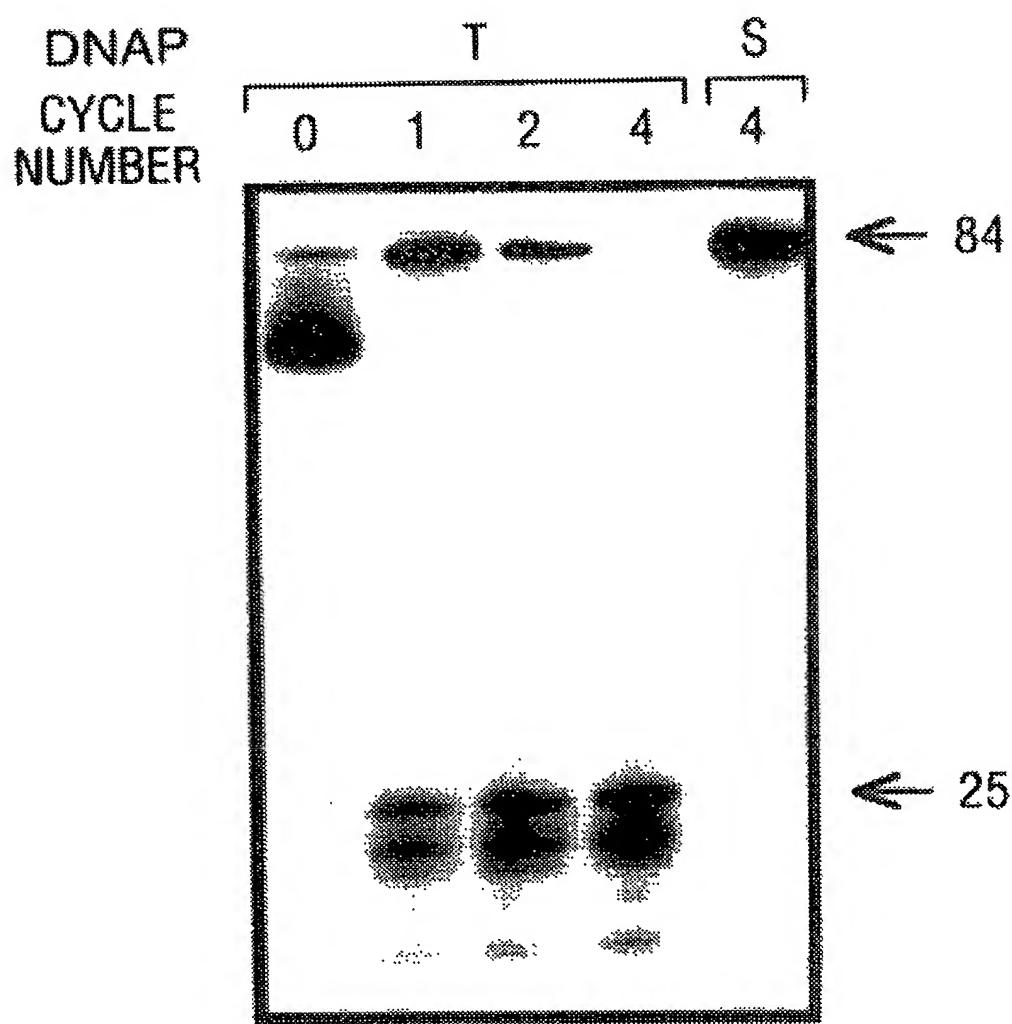


FIG. 8

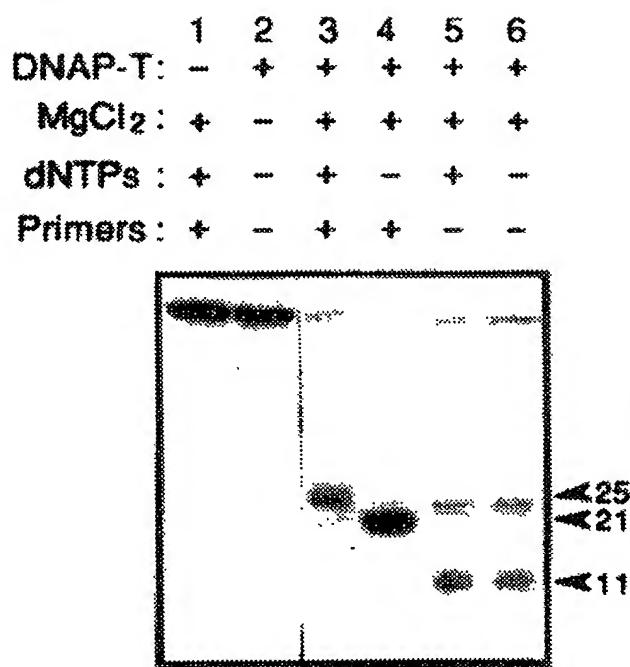


FIG. 9A

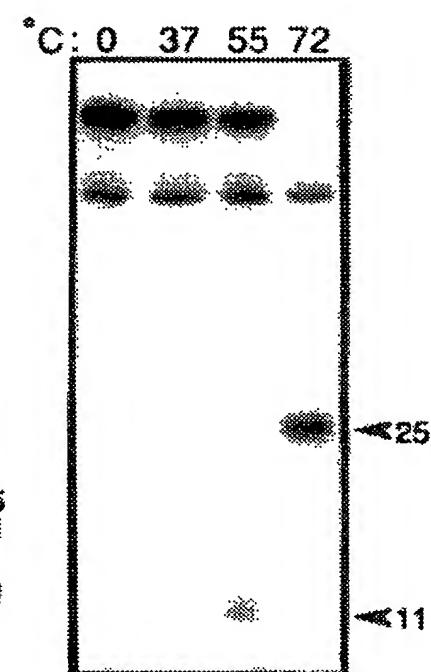


FIG. 9B

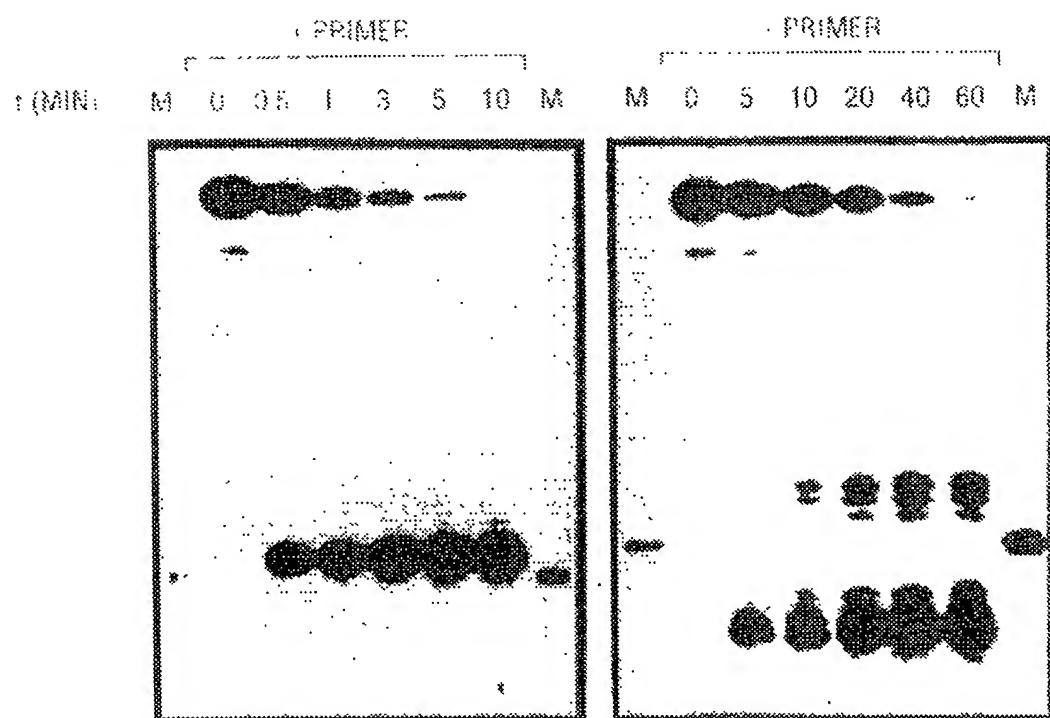


FIG. 10A

FIG. 10B

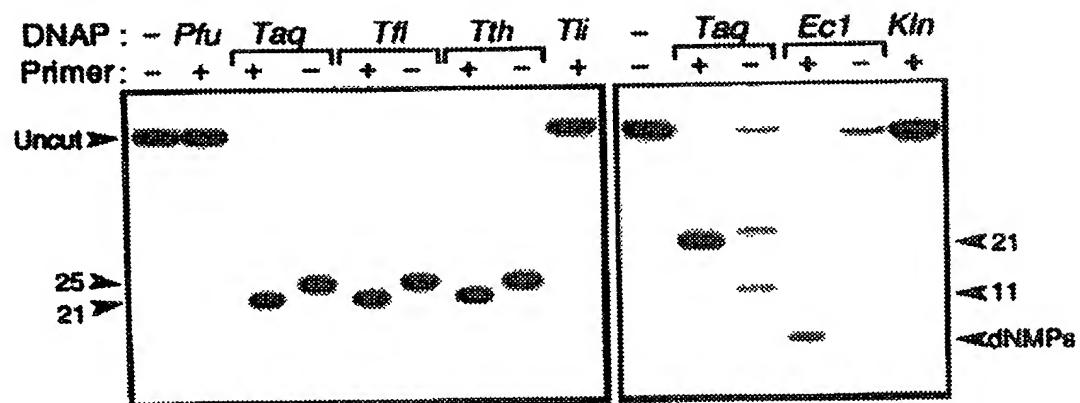
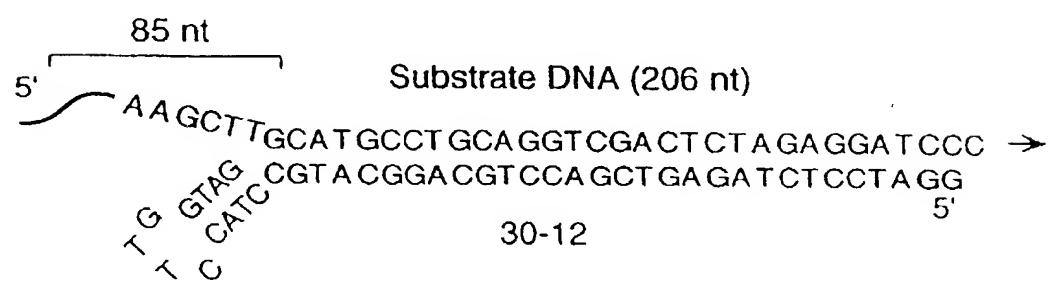
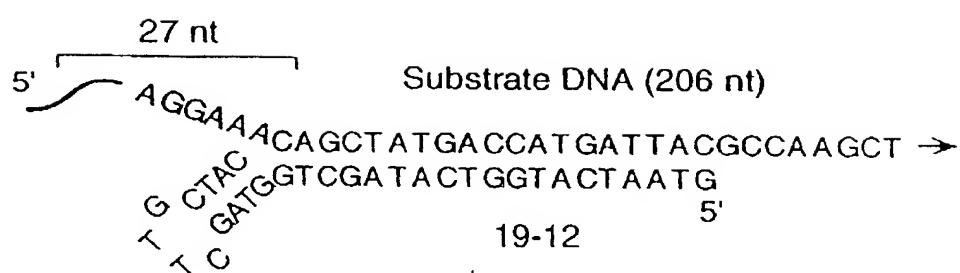


FIG. 11A

FIG. 11B

FIG. 12A



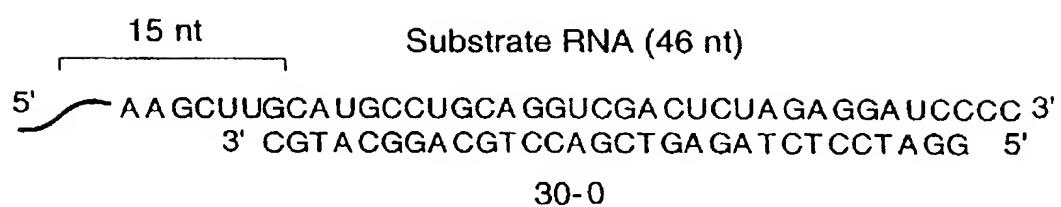


FIG. 13A

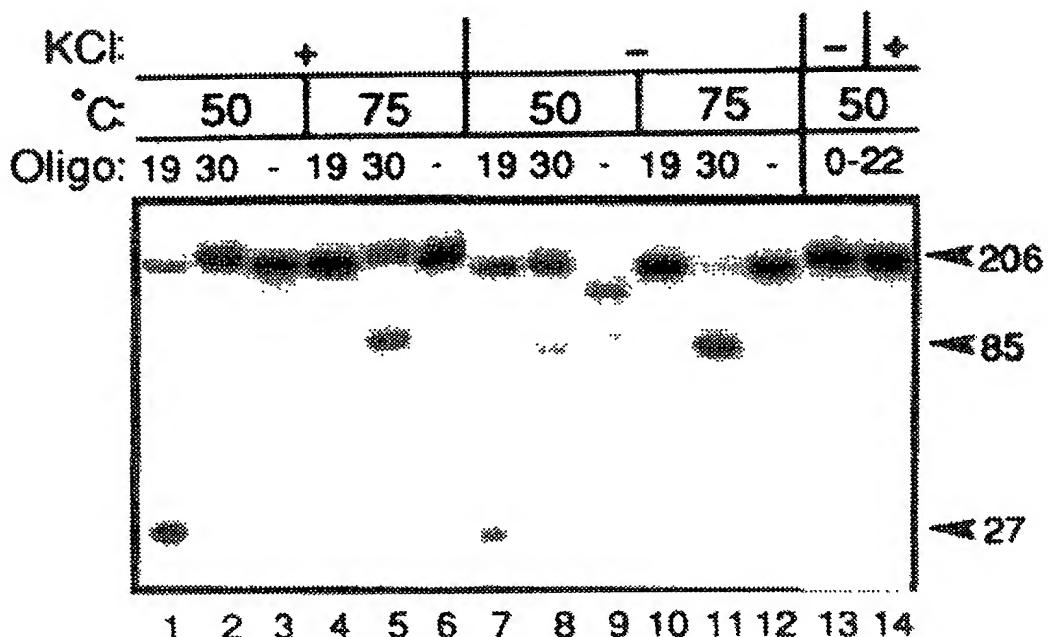


FIG. 12B

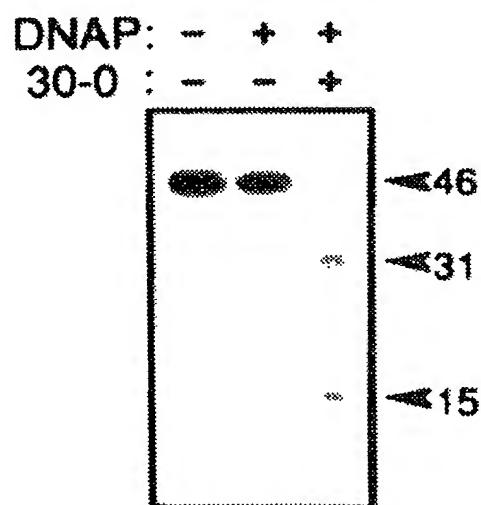


FIG. 13B

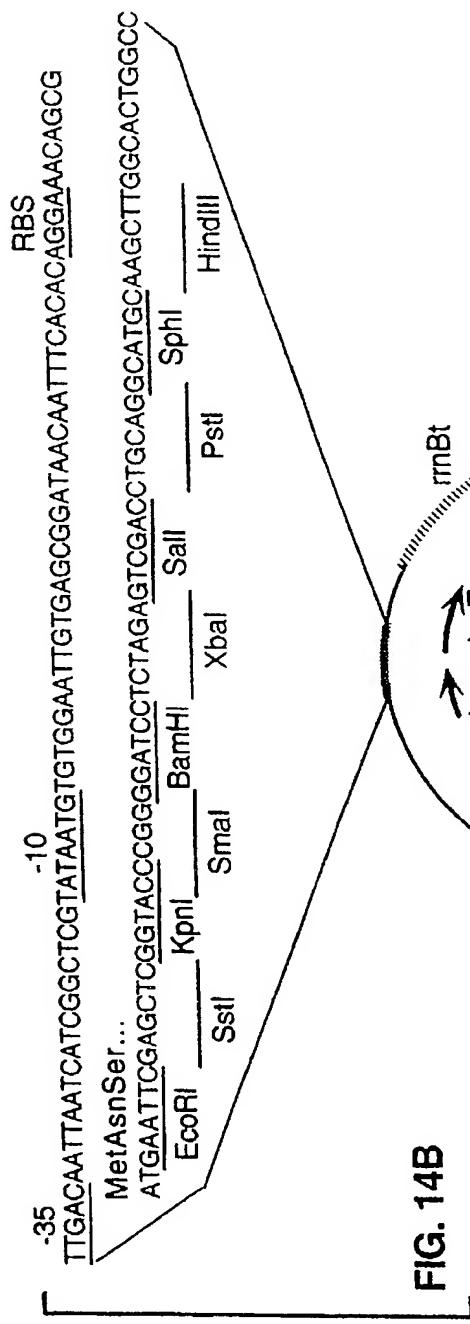


FIG. 14B

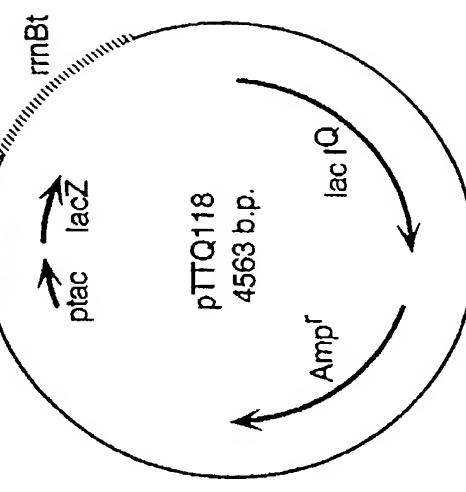
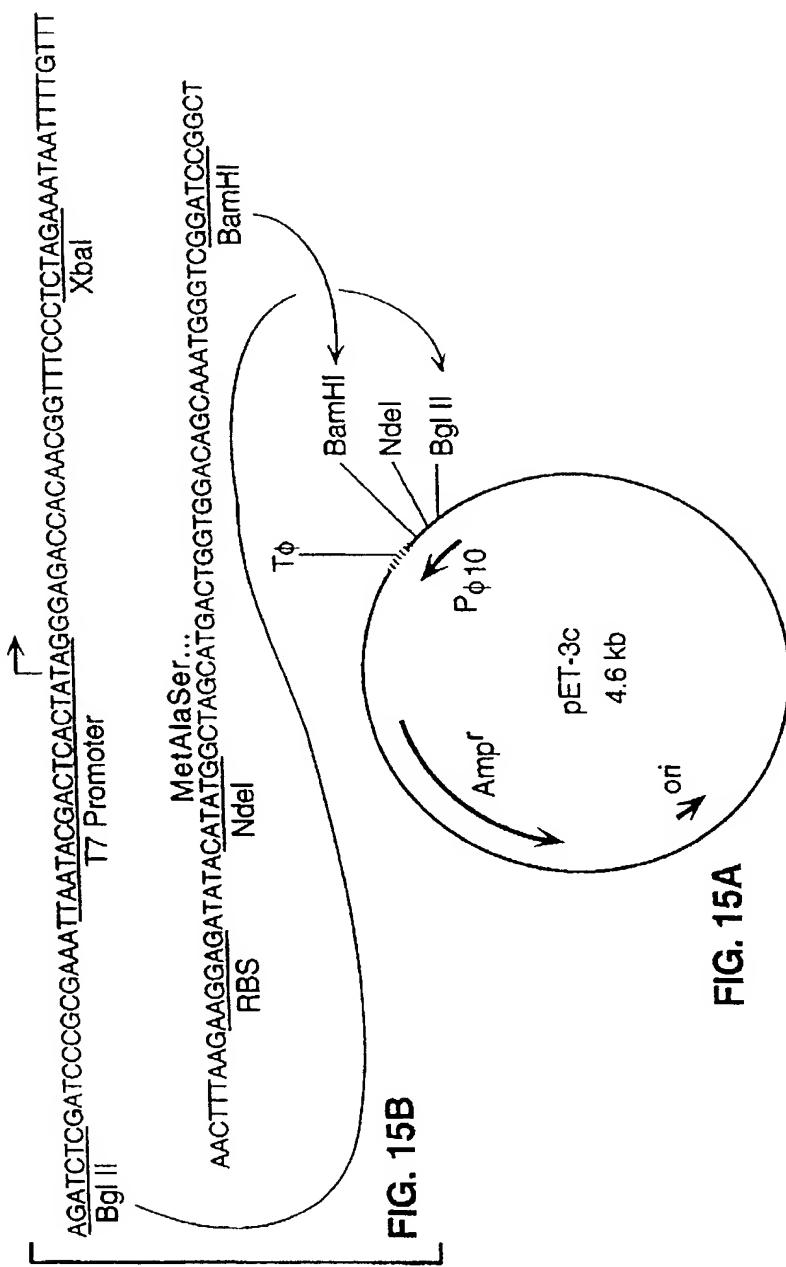


FIG. 14A

RBS: Ribosome binding site
 lacZ: Beta-galactosidase alpha fragment
 ptac: Synthetic tac promoter
 rmBt: E. coli rmB transcription terminator
 lacIQ: Lac repressor gene

FIG. 14C



$P\phi 10$: Bacteriophage $T7\phi 10$ promoter
 $T\phi$: $T7\phi$ Terminator
RBS: Ribosome binding site

FIG. 15C

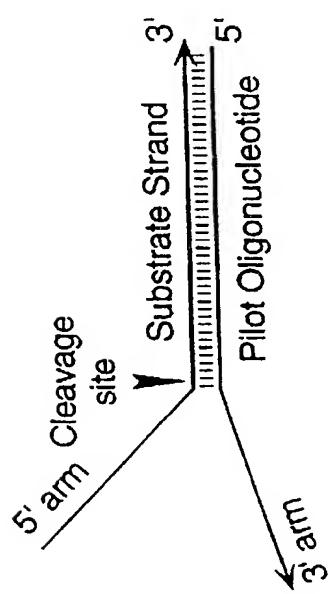


FIG. 16A

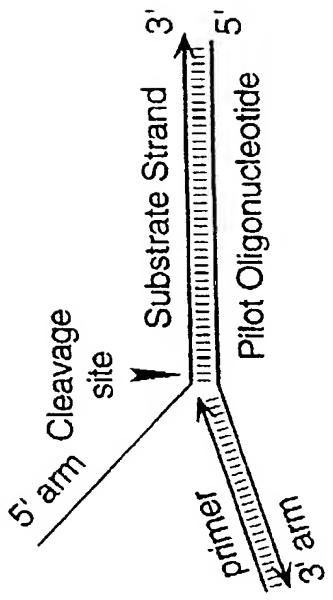


FIG. 16B

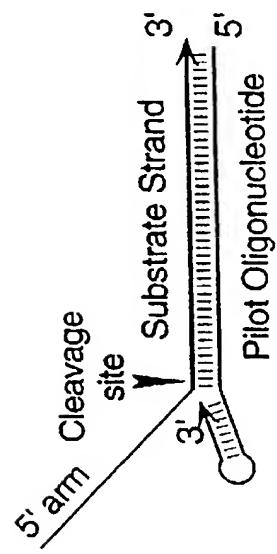


FIG. 16C

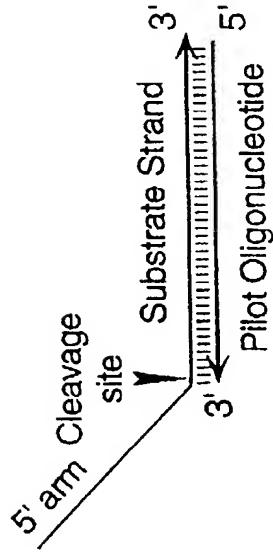


FIG. 16D

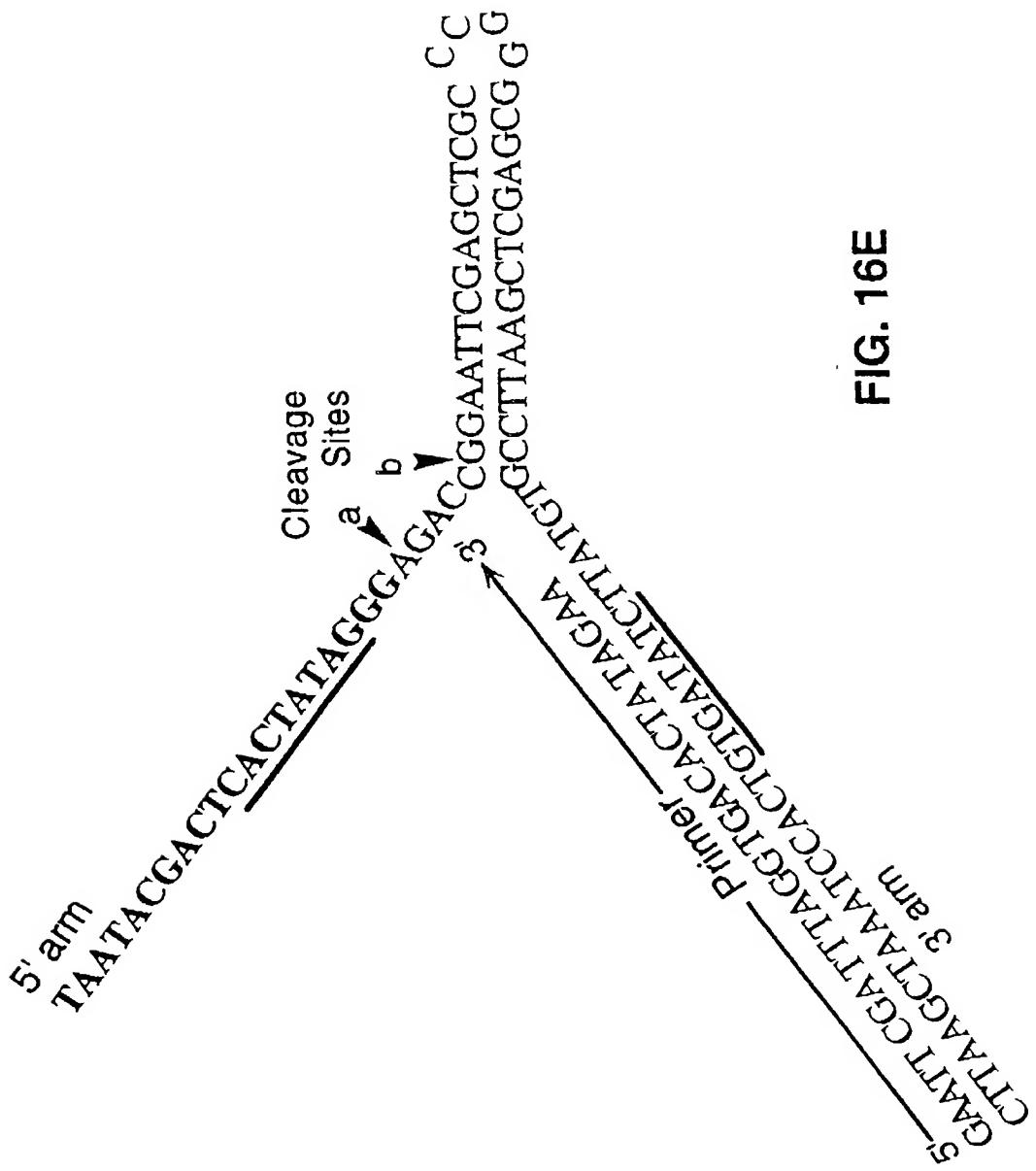


FIG. 16E

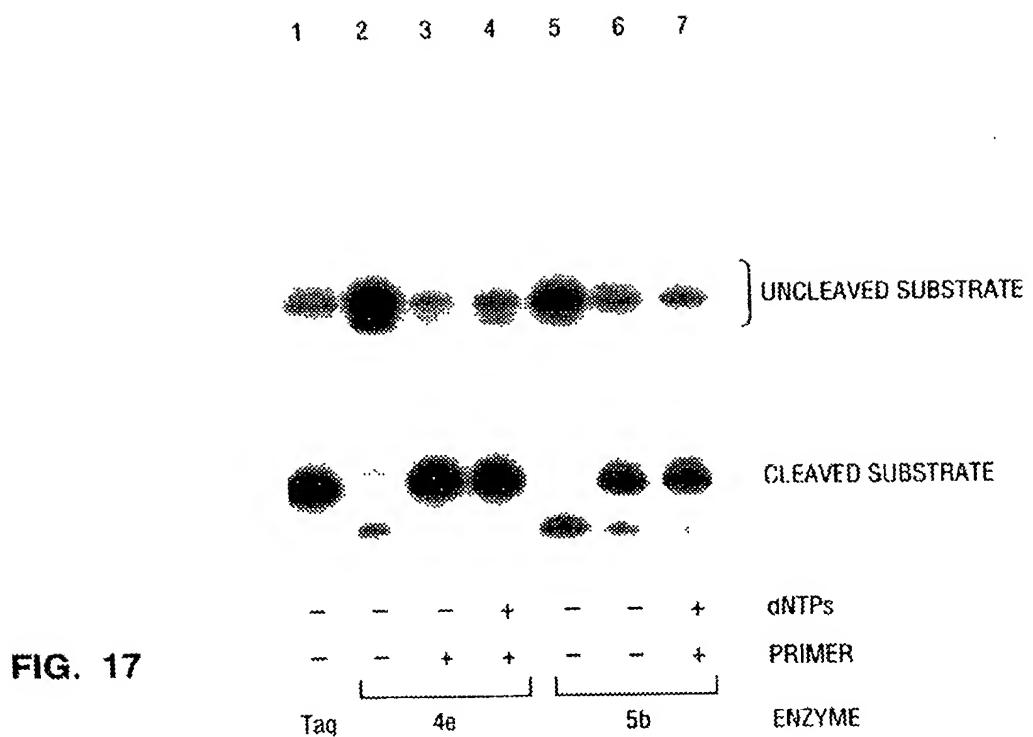


FIG. 17

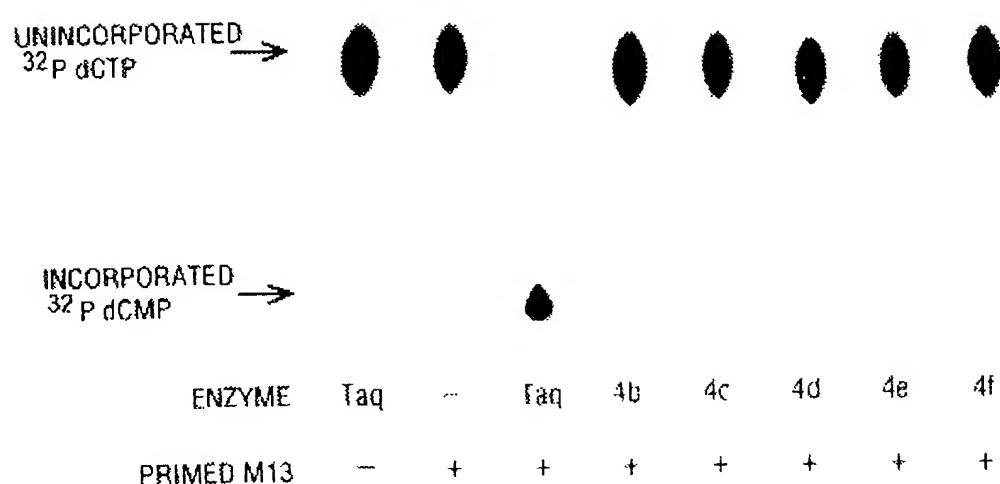


FIG. 18

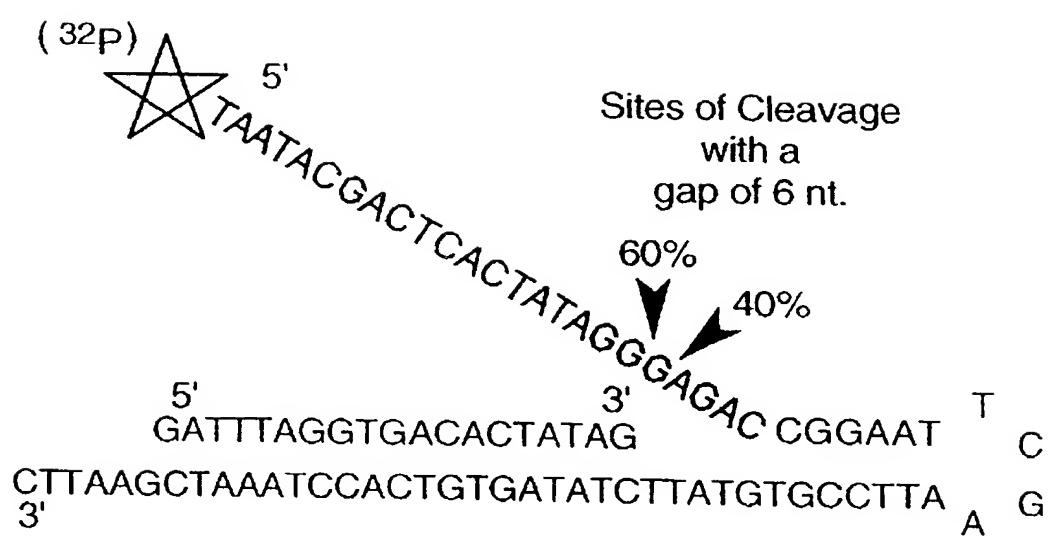
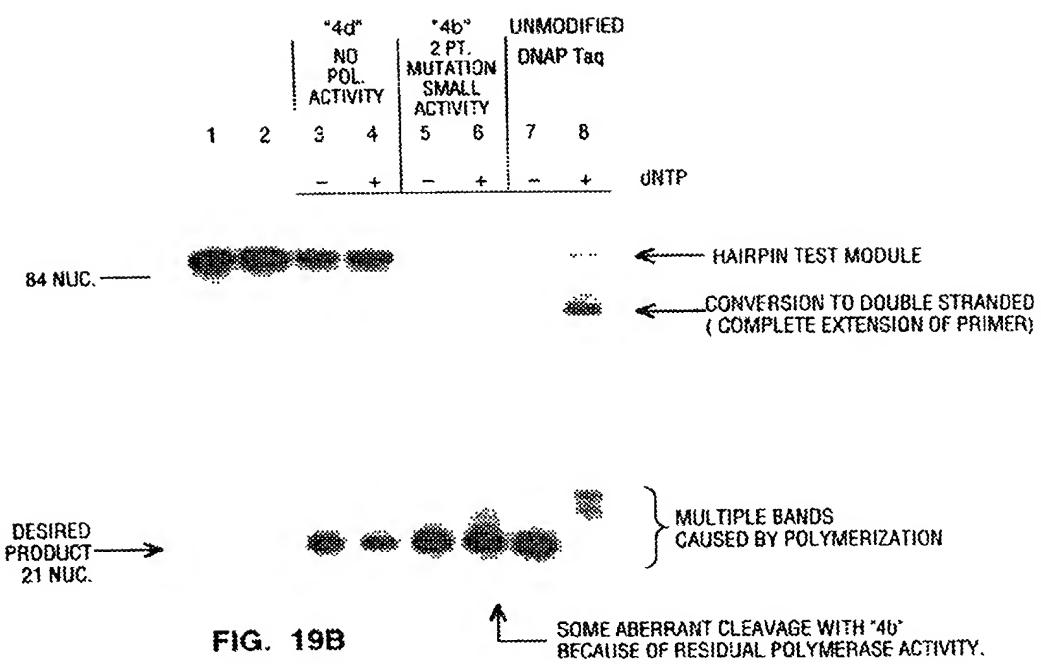


FIG. 19A



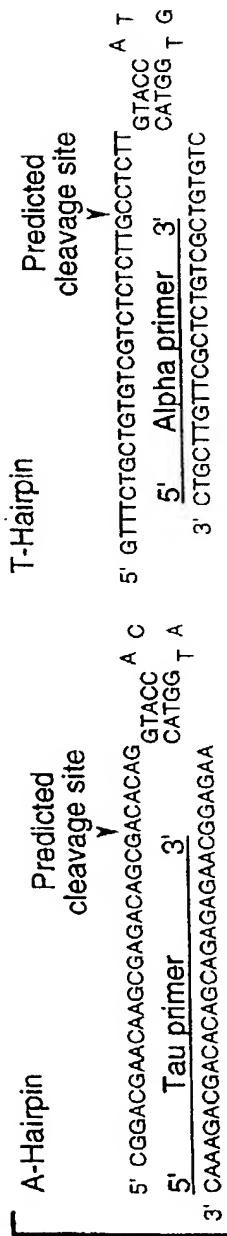


FIG. 20A

Sequence of alpha primer:
 5' GACGAACAAAGCGAGACAGCAGCG 3'

FIG. 20B

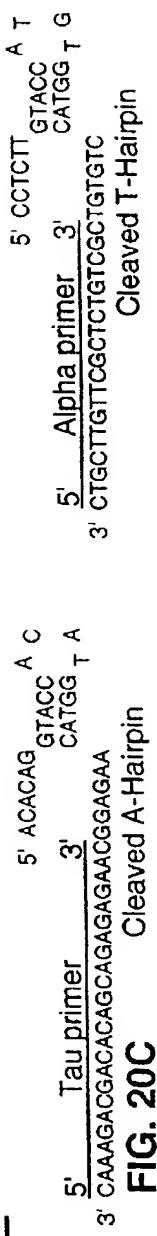


FIG. 20C

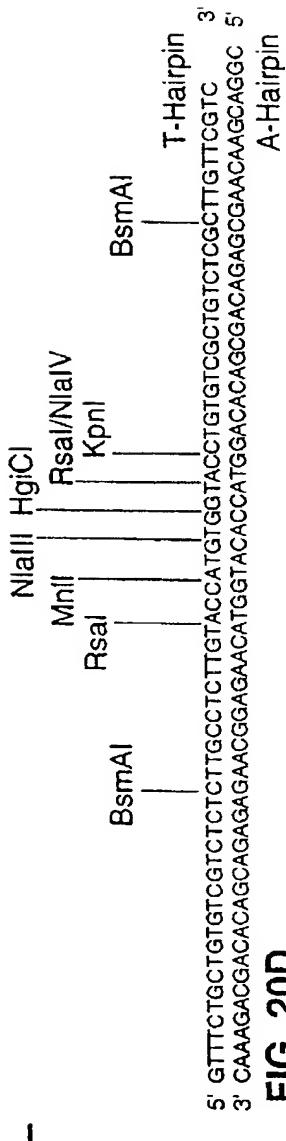


FIG. 20D



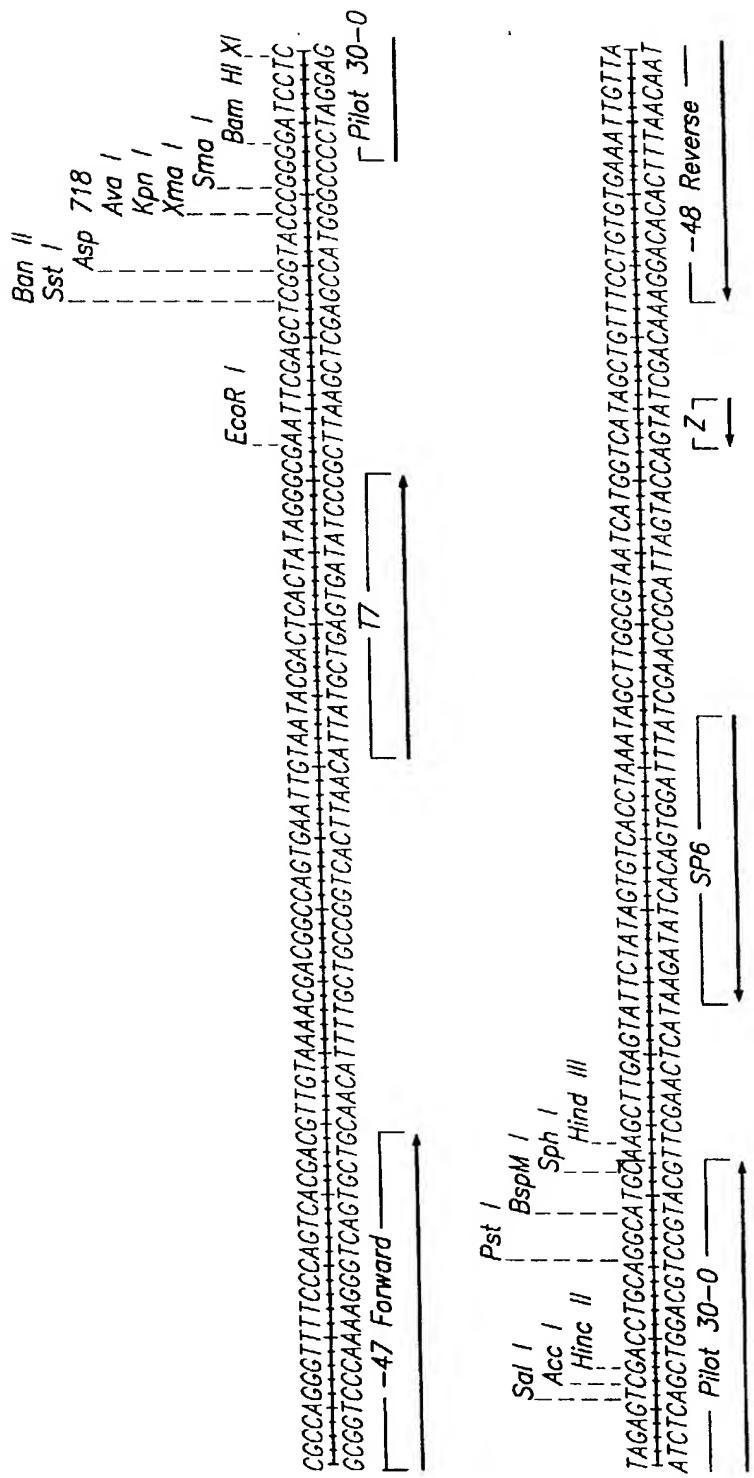


FIG. 21

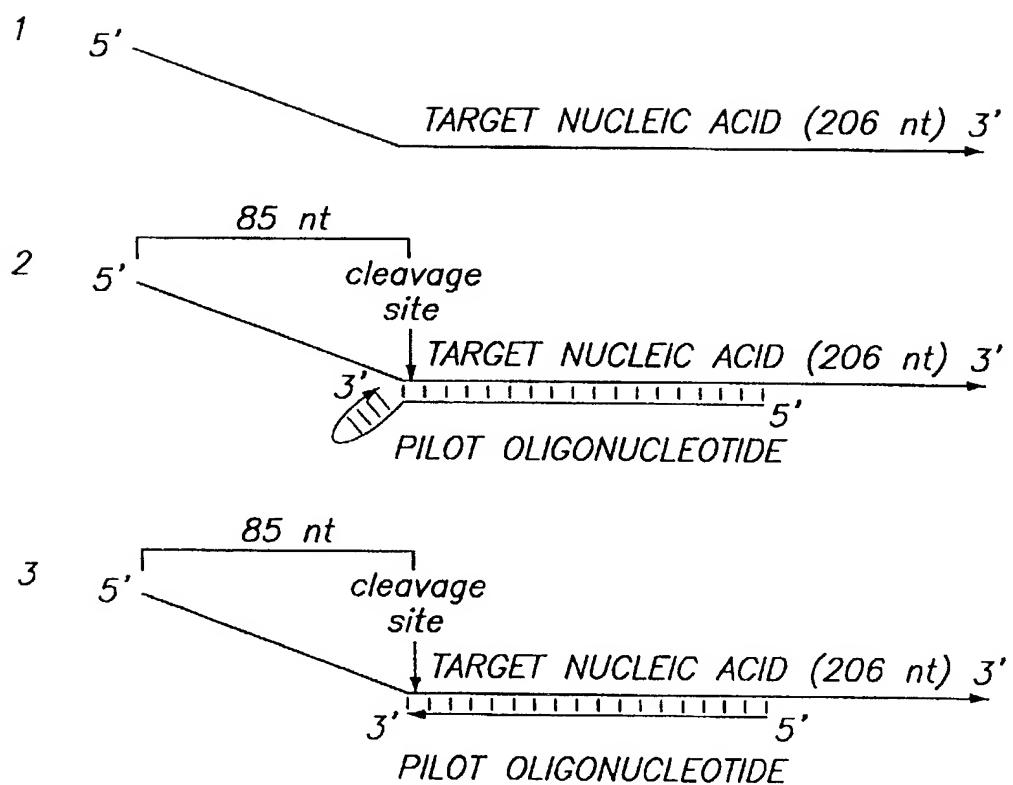


FIG. 22A

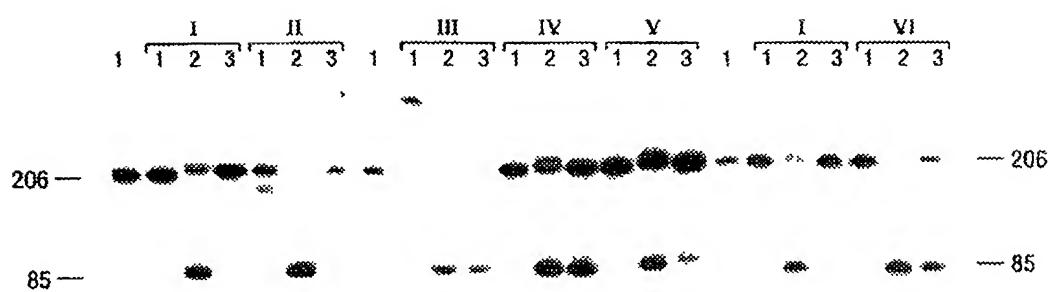


FIG. 22B

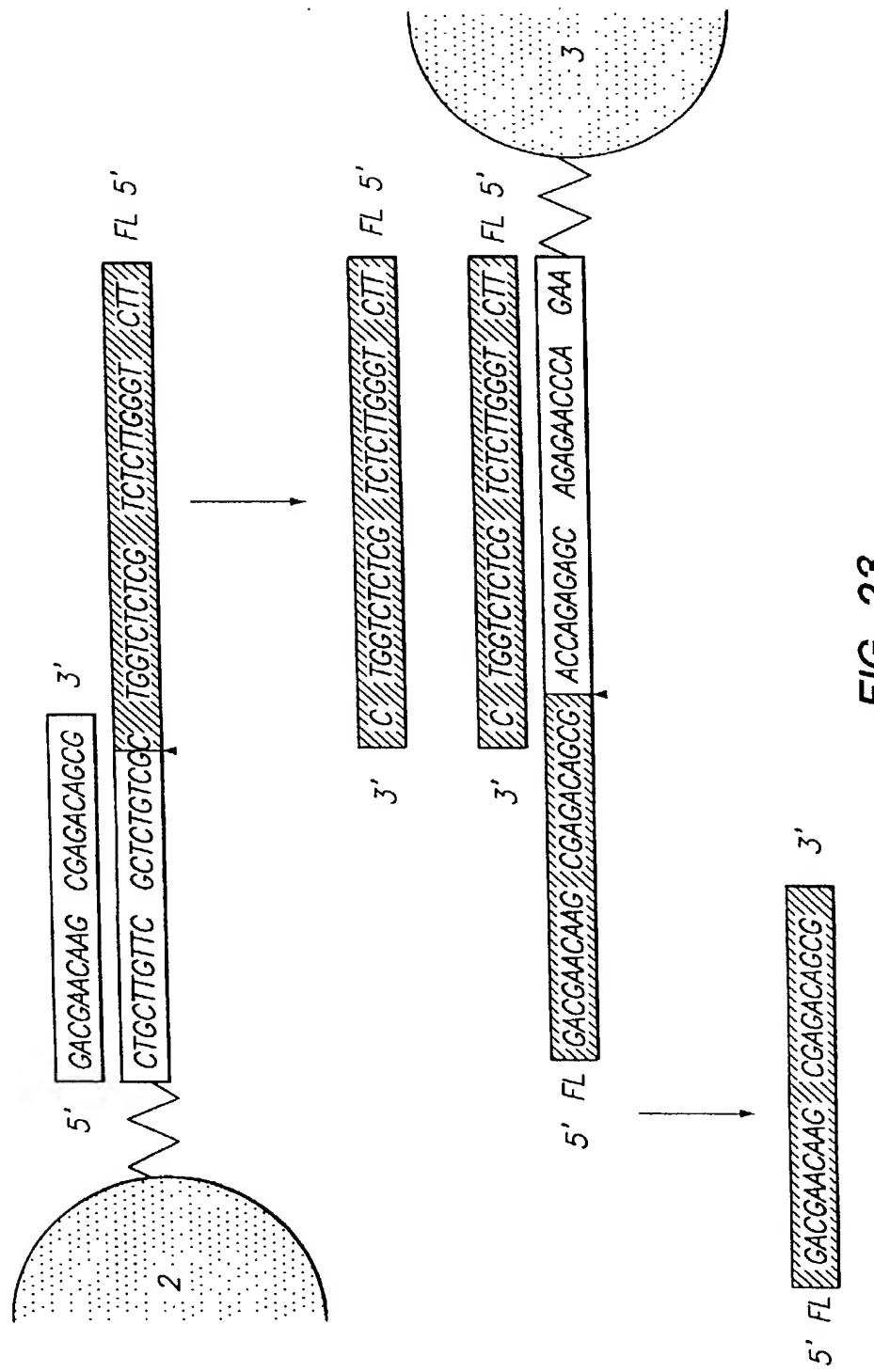


FIG. 23

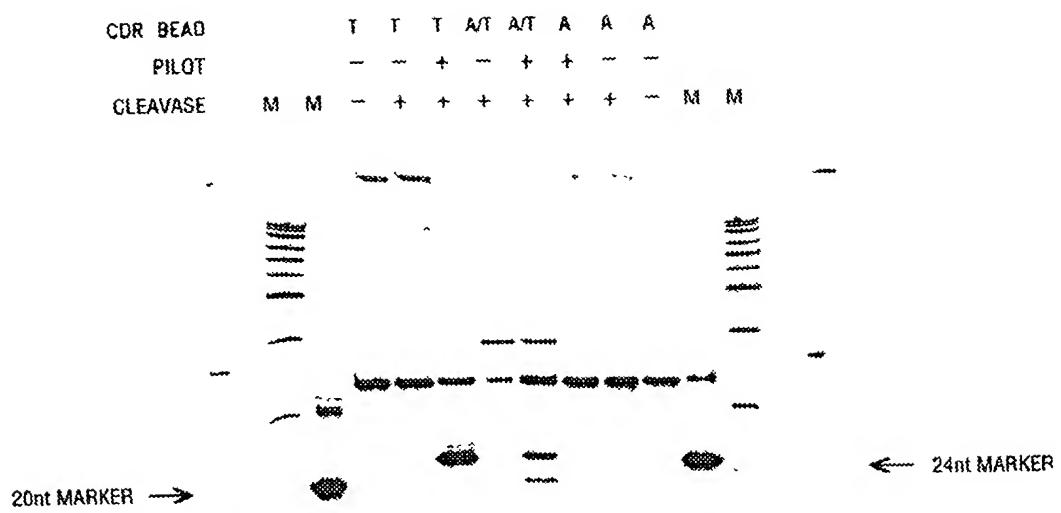


FIG. 24

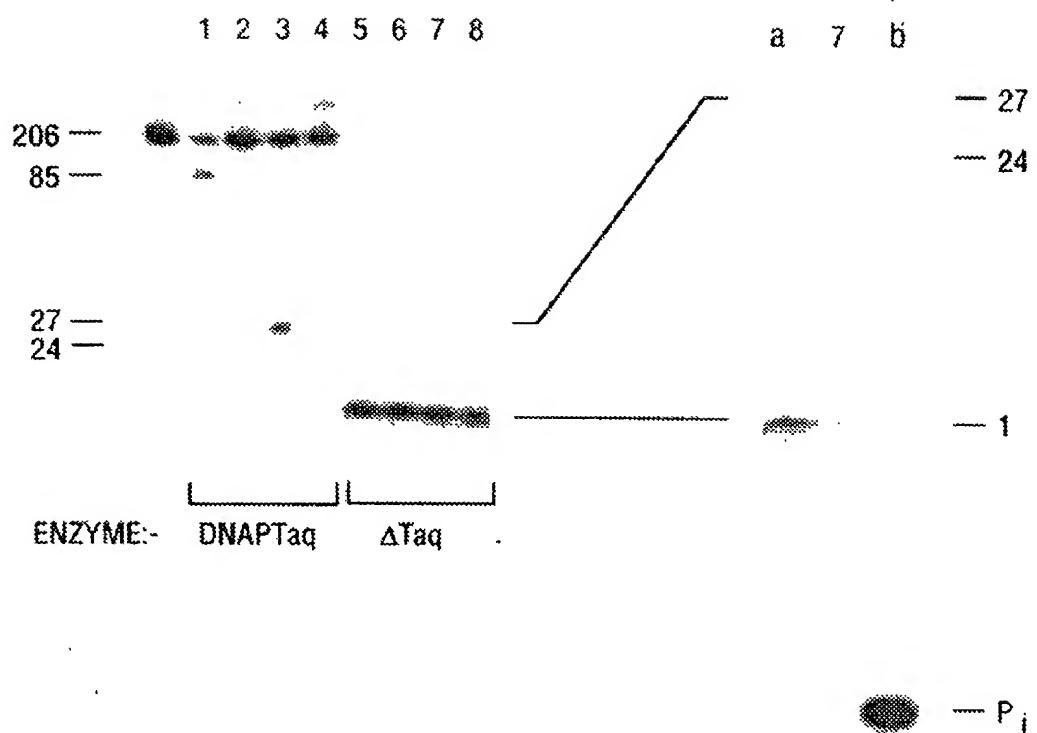
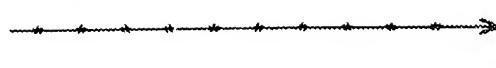


FIG. 25A

FIG. 25B

FIG. 26A



— 206

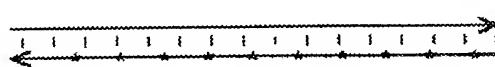


FIG. 26B

* = 32P

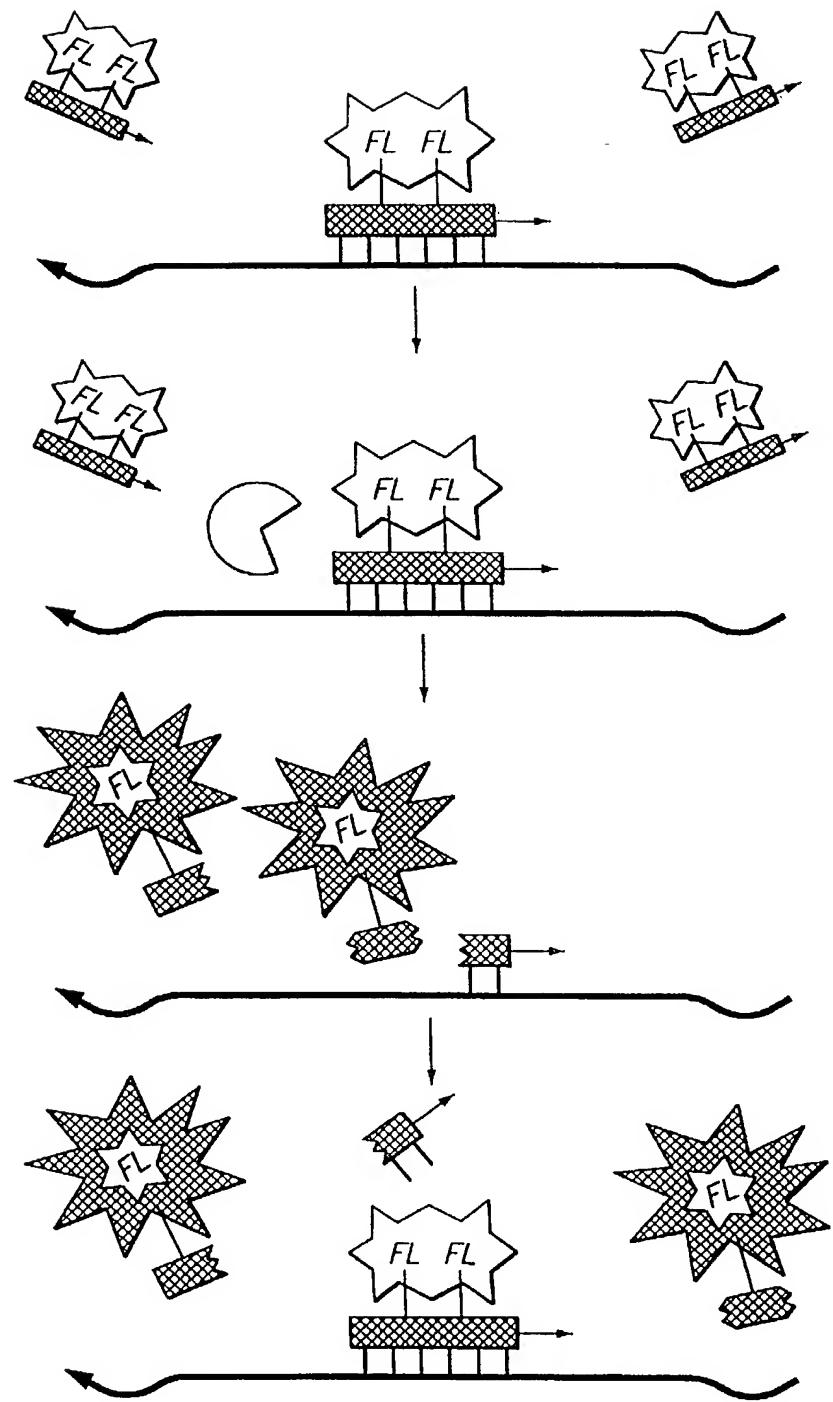


FIG. 27

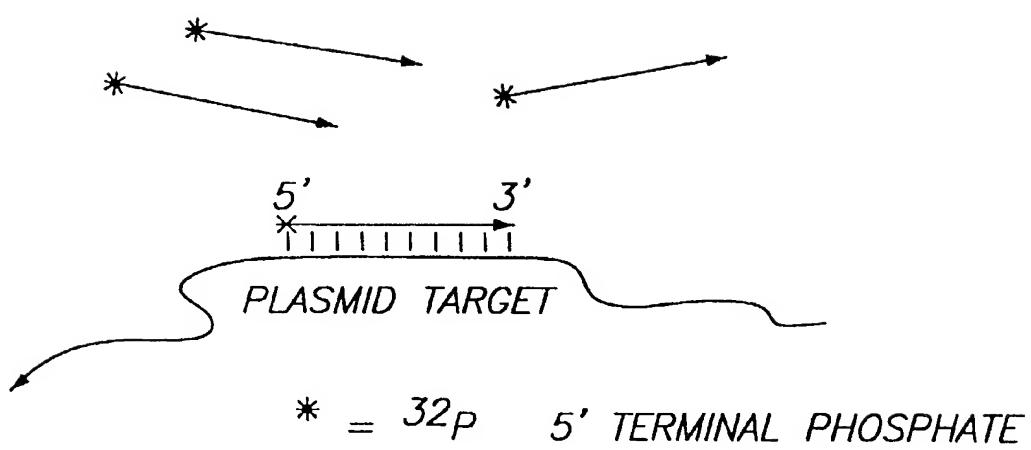


FIG. 28A

M 1 2 3 4 5 6

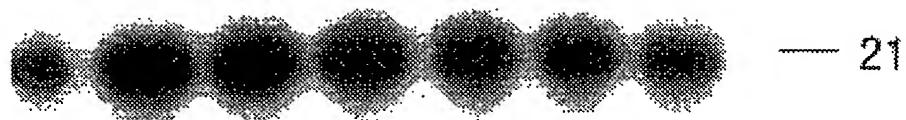


FIG. 28B

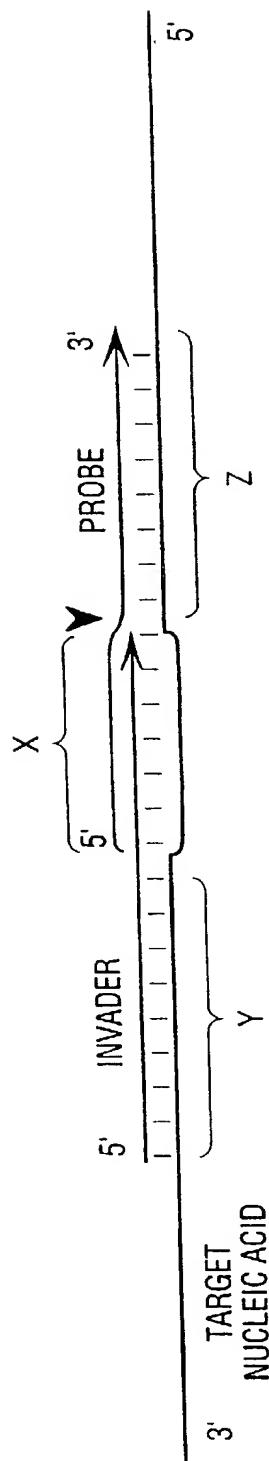


FIG. 29

FIG. 30

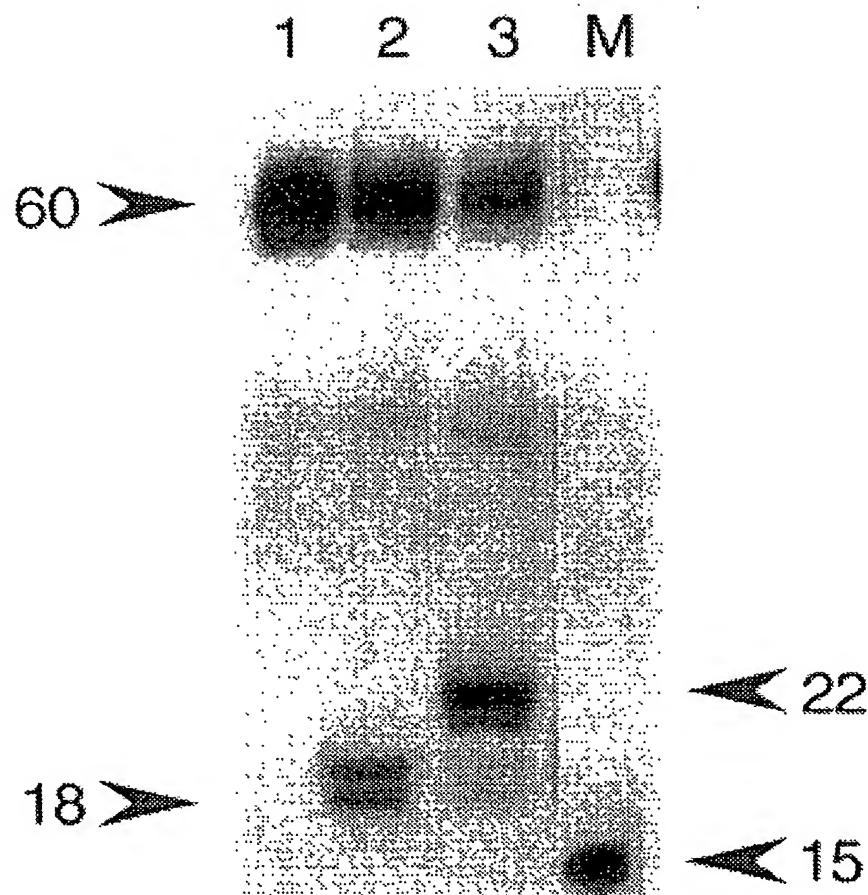


FIG. 31

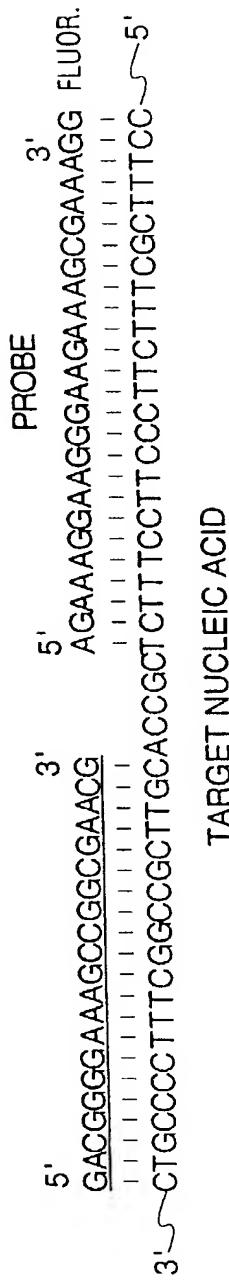


FIG. 32A

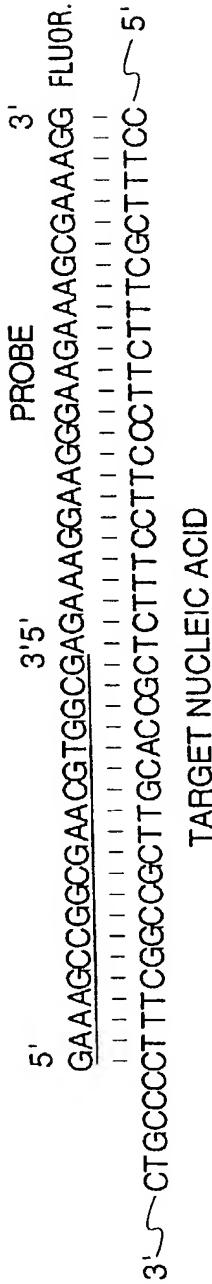
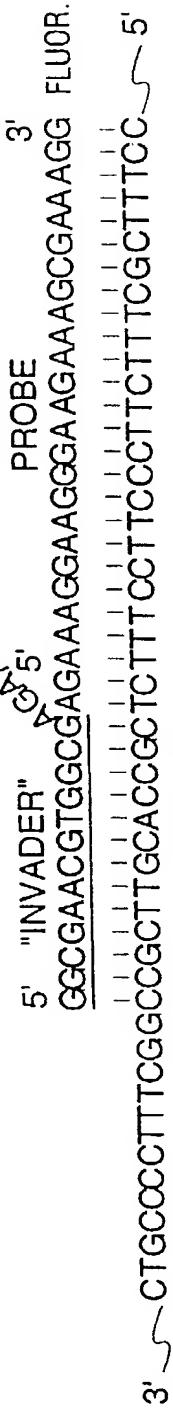


FIG. 32B



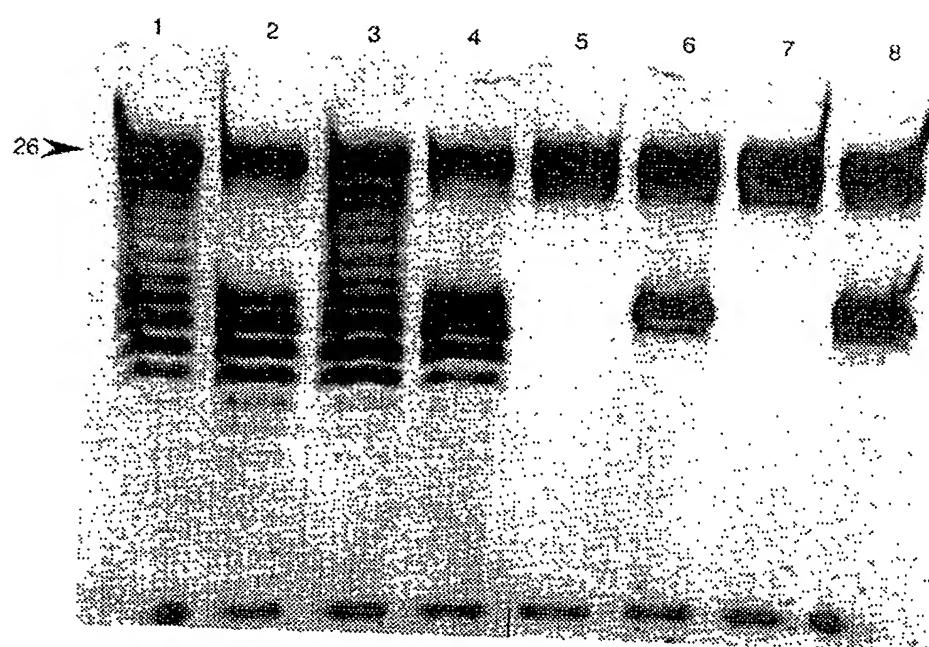


FIG. 33

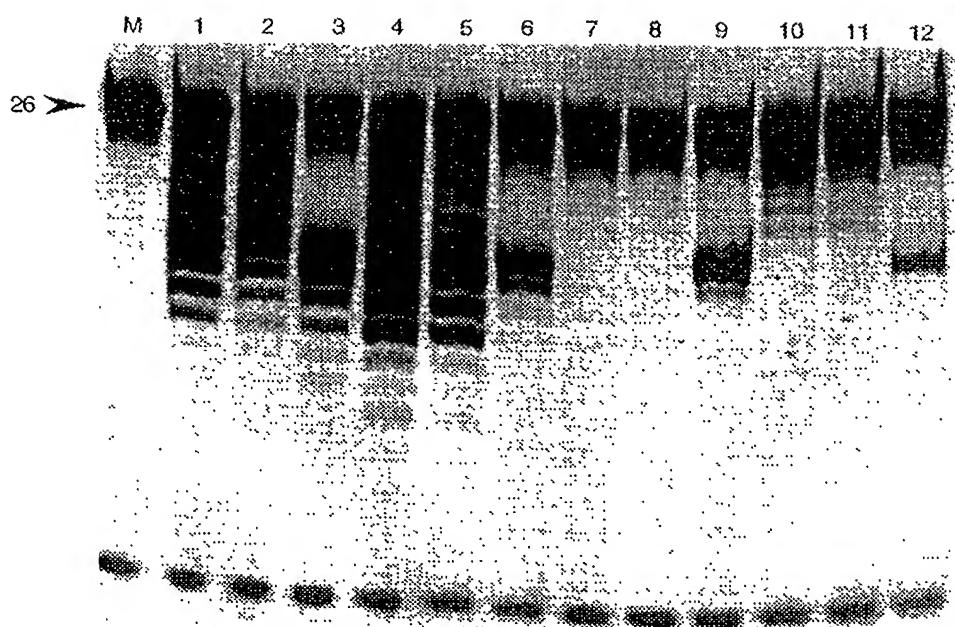


FIG. 34

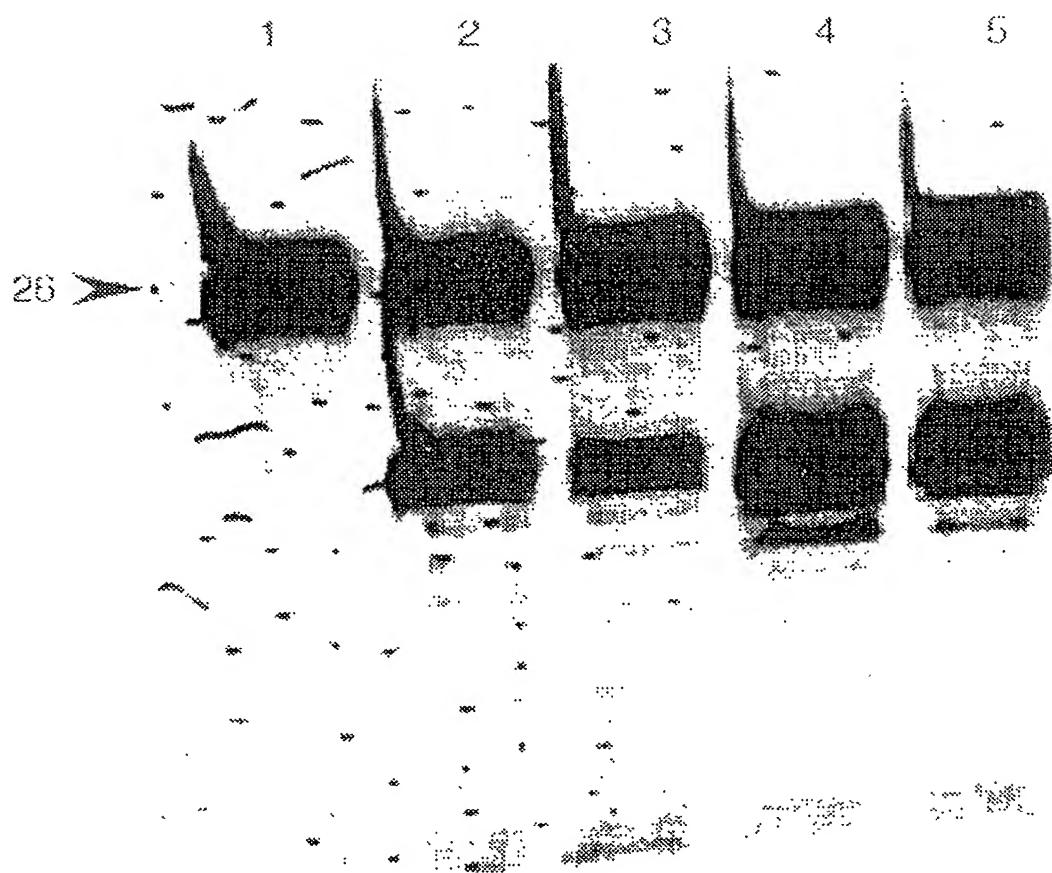


FIG. 35

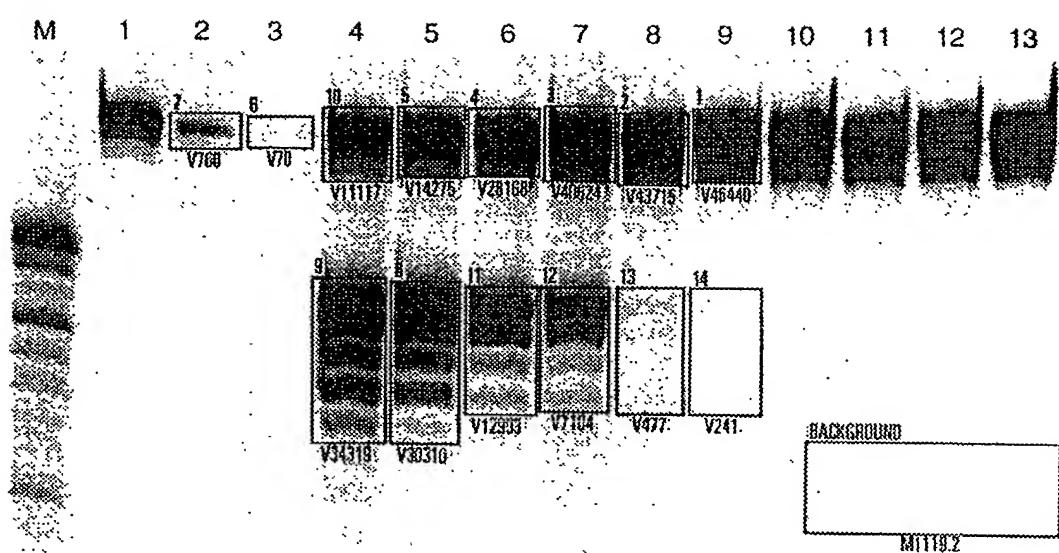


FIG. 36

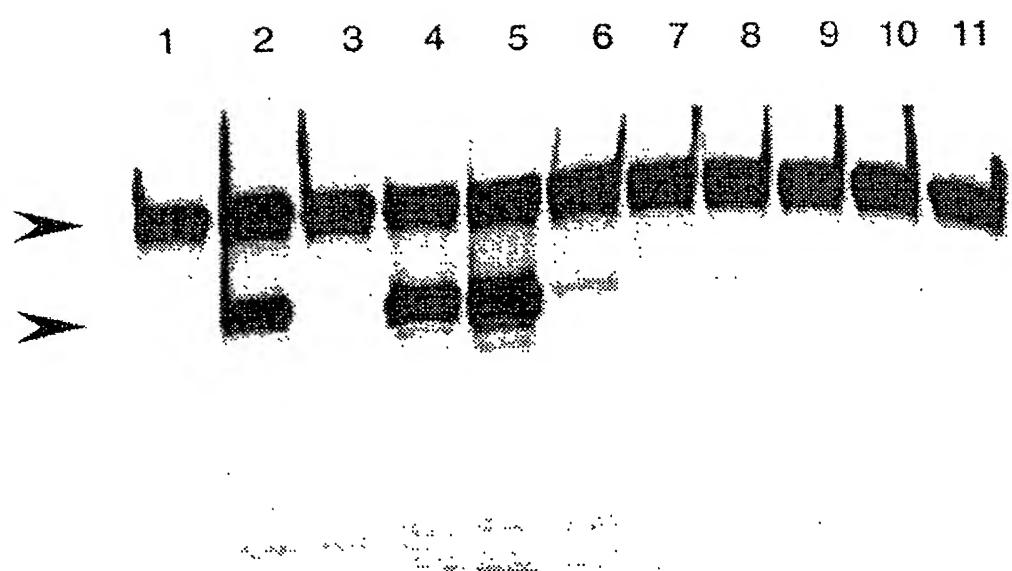


FIG. 37

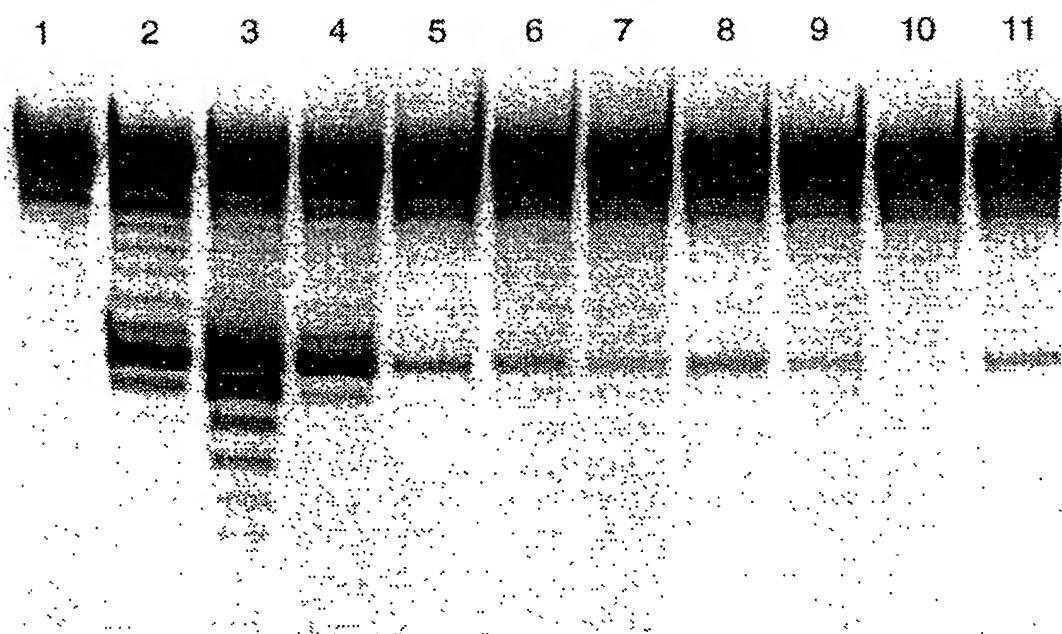


FIG. 38

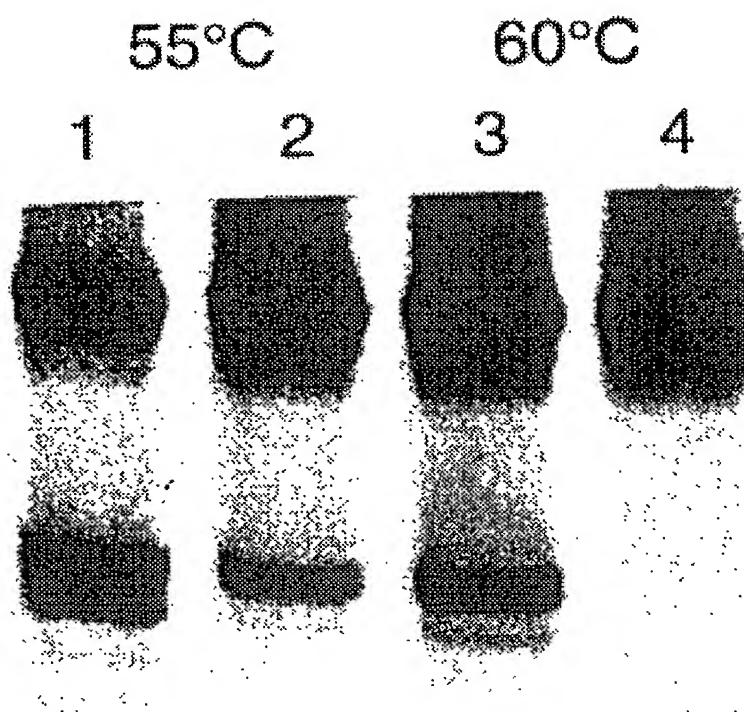


FIG. 39

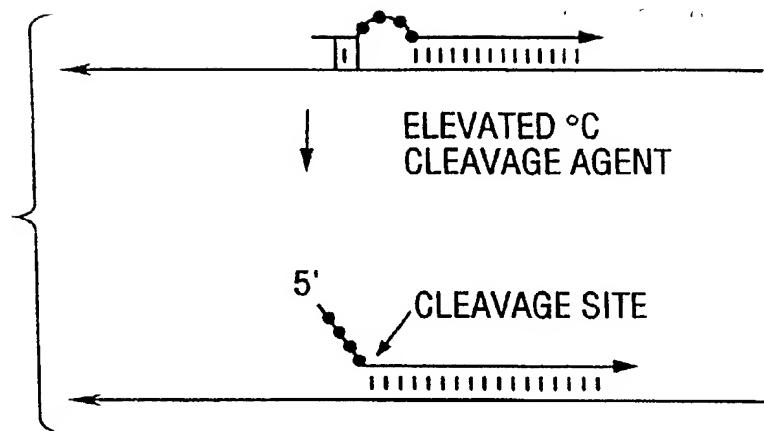


FIG. 40A

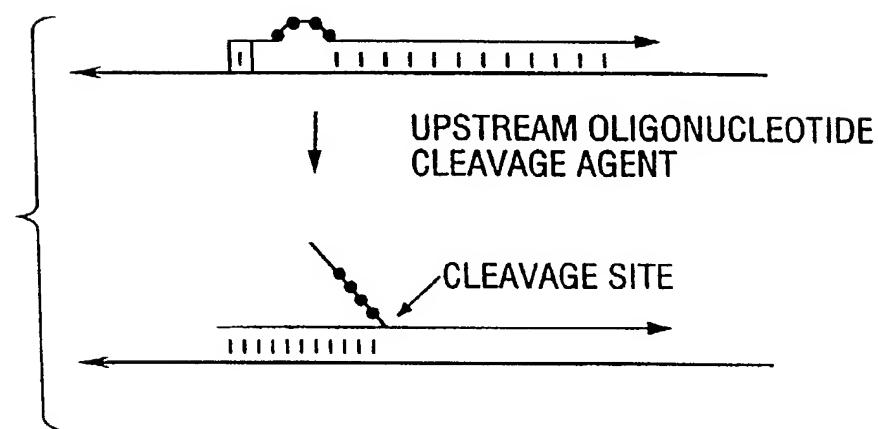


FIG. 40B

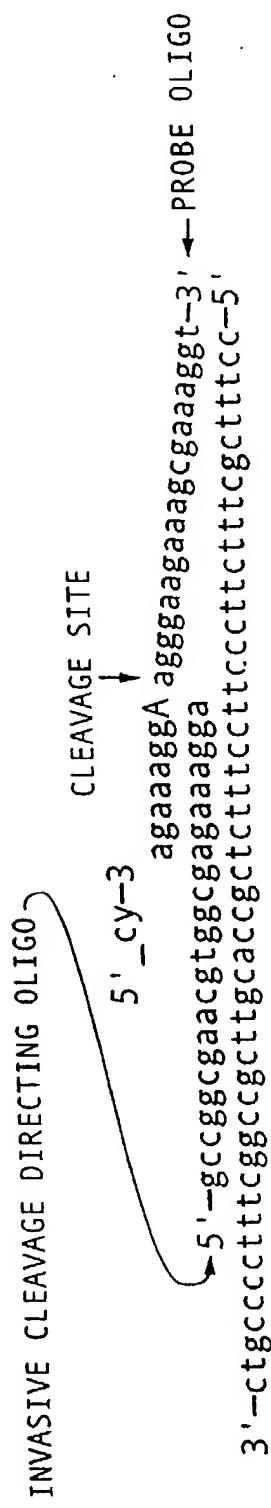


FIG. 41

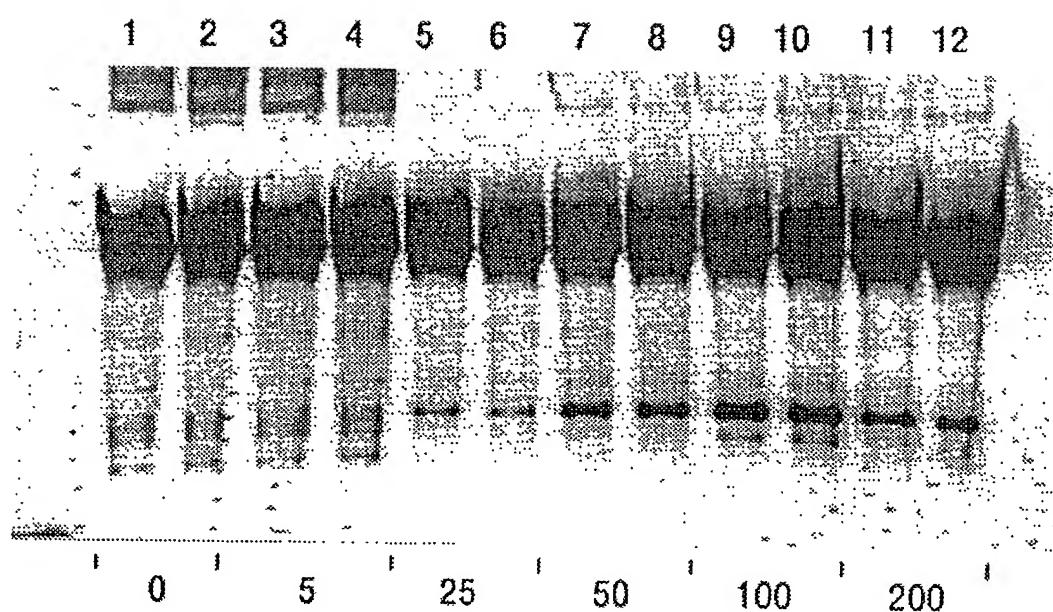


FIG. 42

1 2 3 4 5 6 7 8 9 10

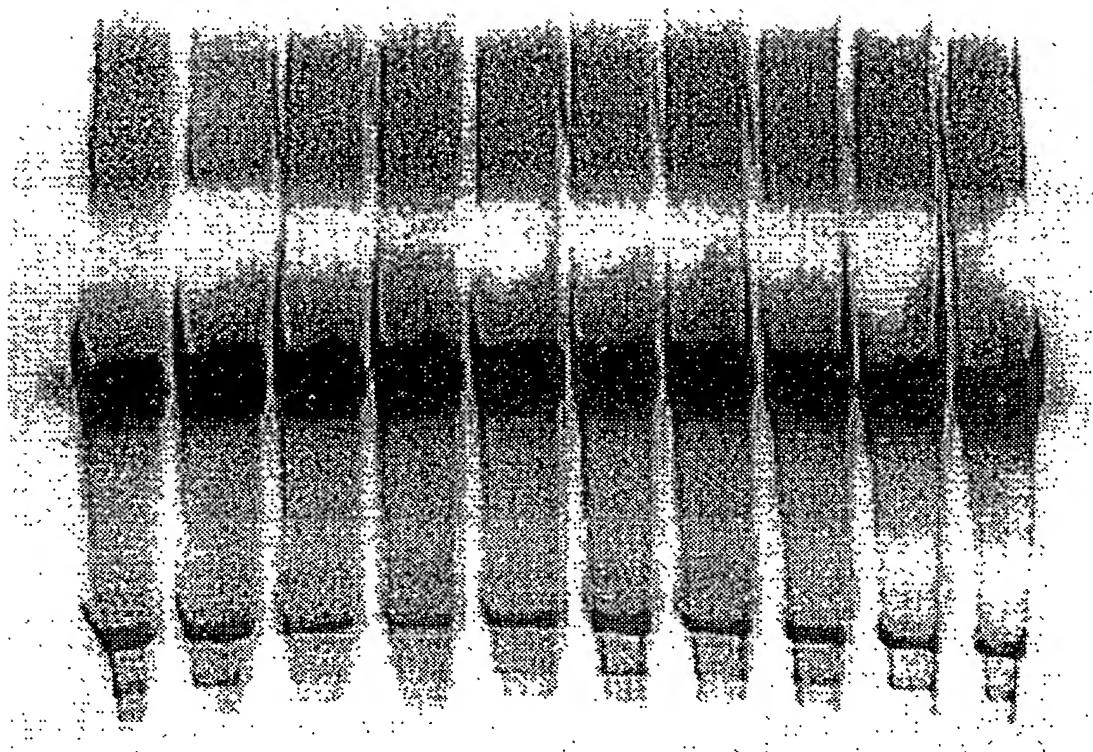


FIG. 43

1 2 3 4 5 6 7 8 9 10 11 12 13 14

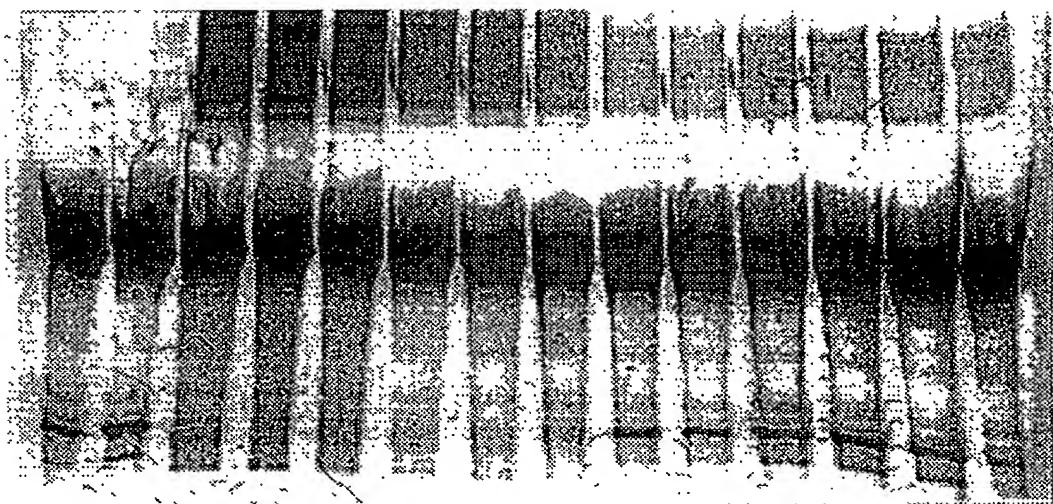


FIG. 44

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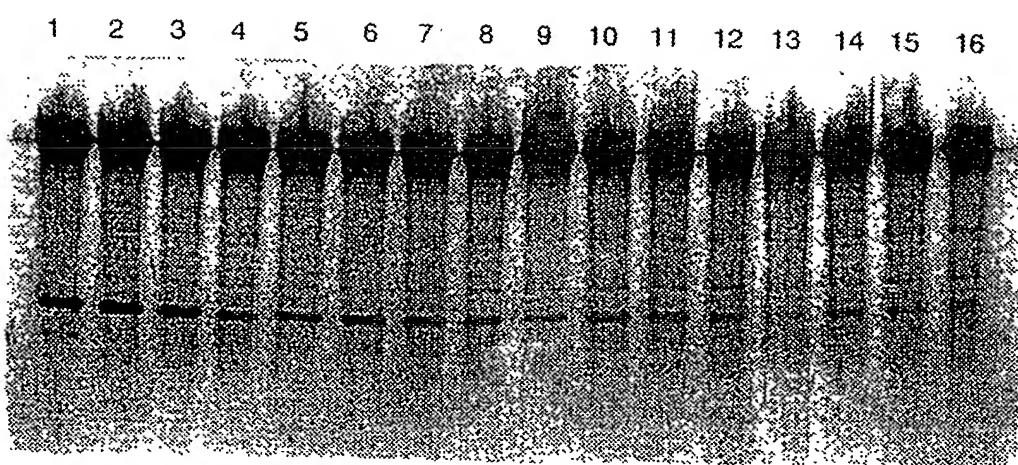


FIG. 45

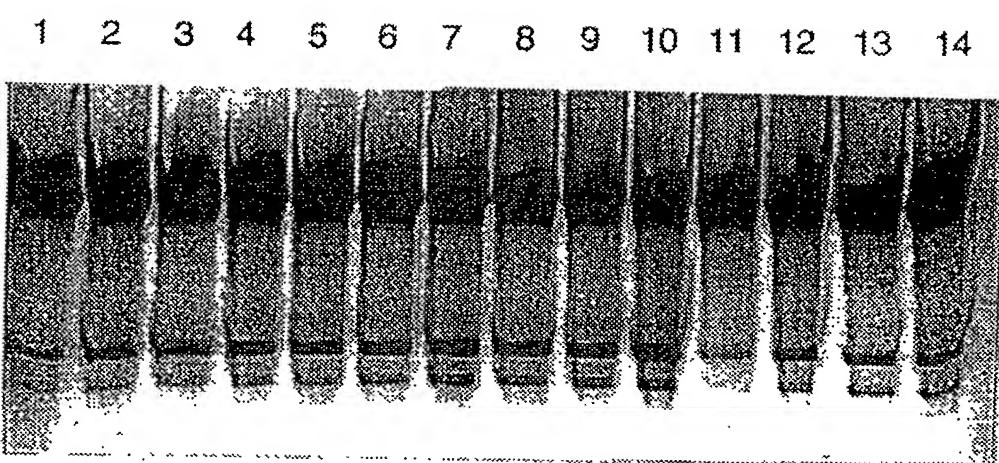


FIG. 46

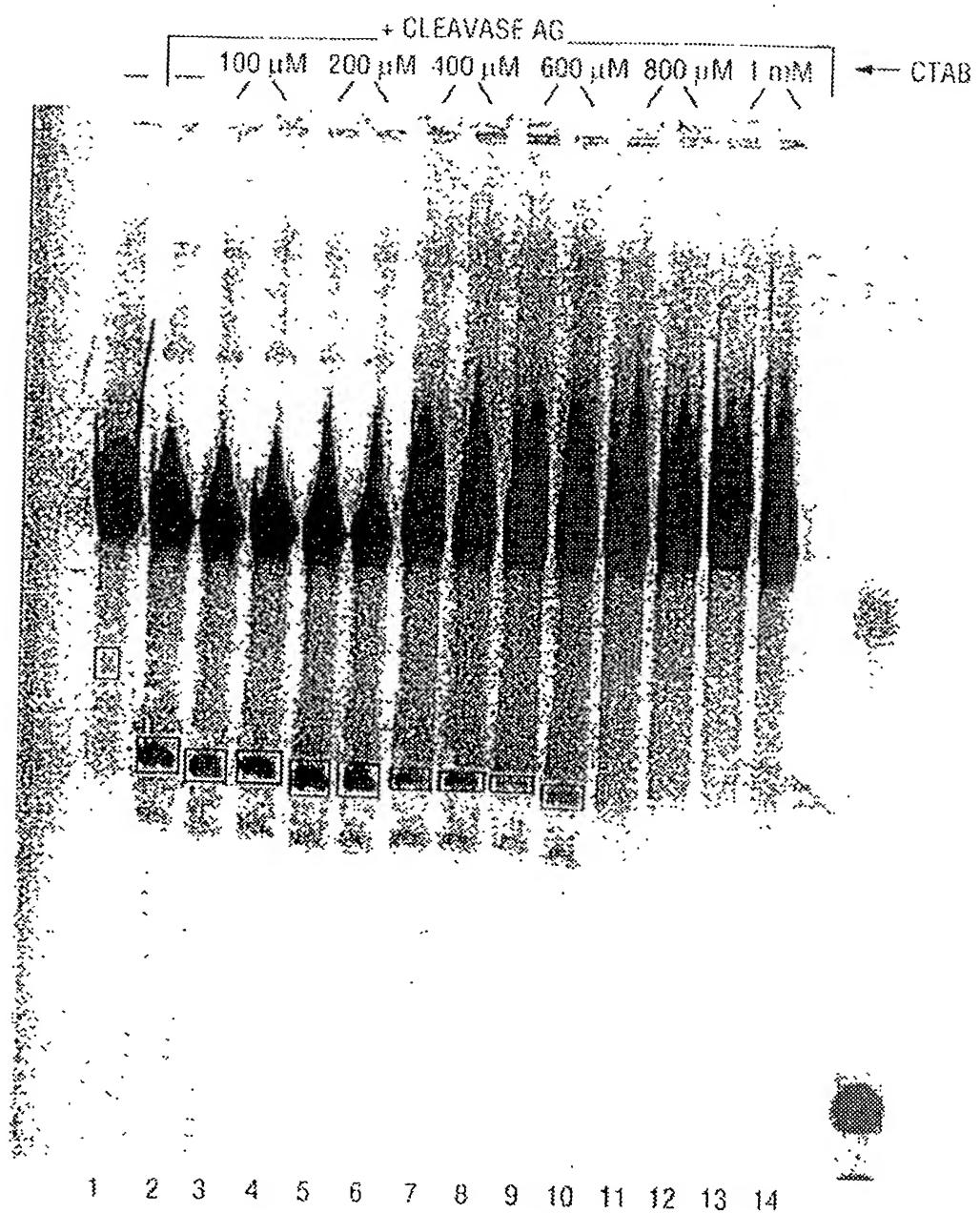


FIG. 47

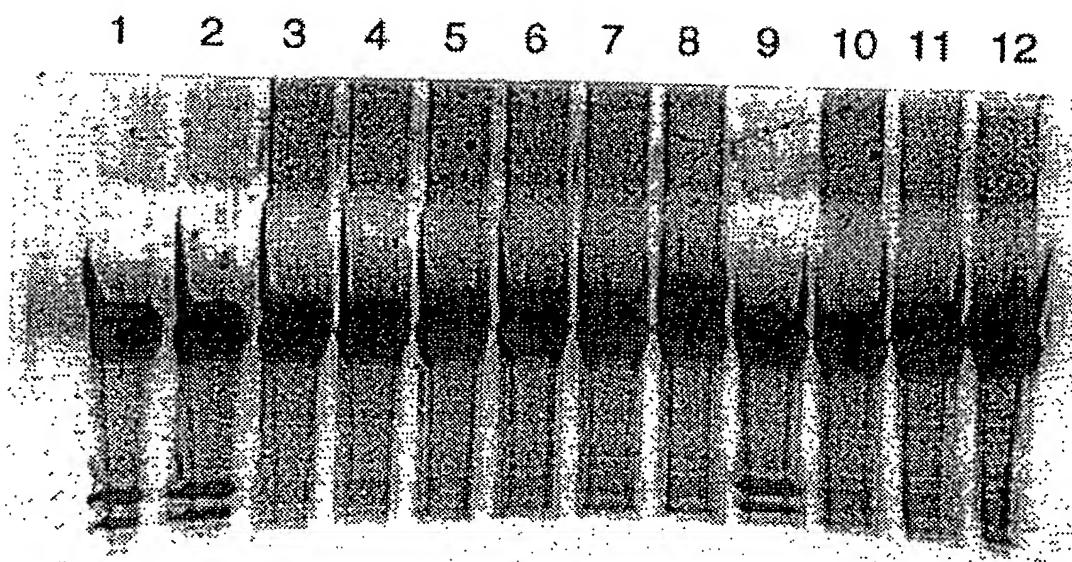


FIG. 48

1 2 3 4 5 6 7 8

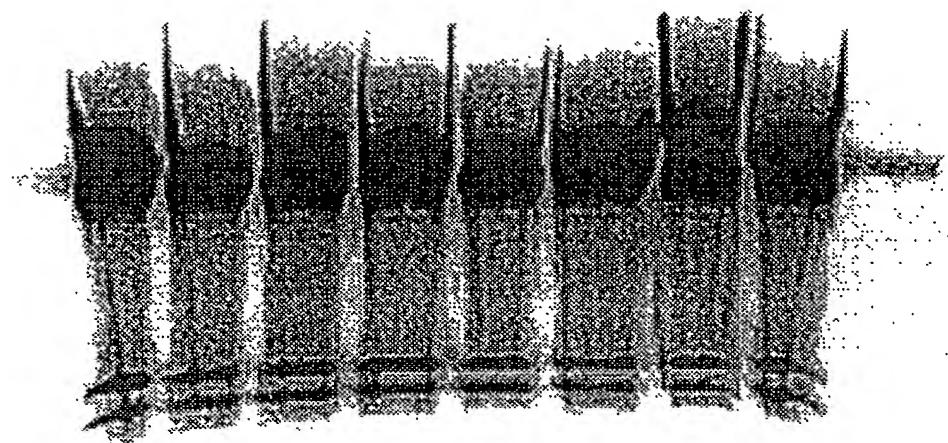


FIG. 49

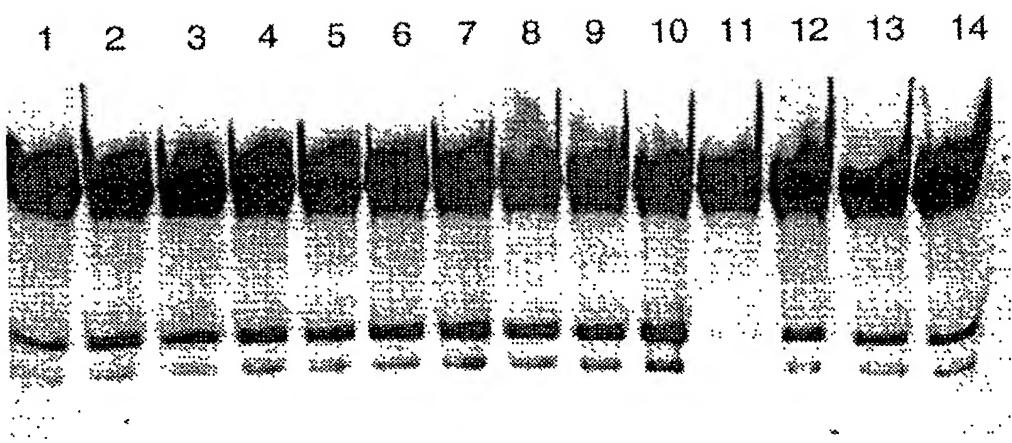


FIG. 50

1 2 3 4 5 6 7

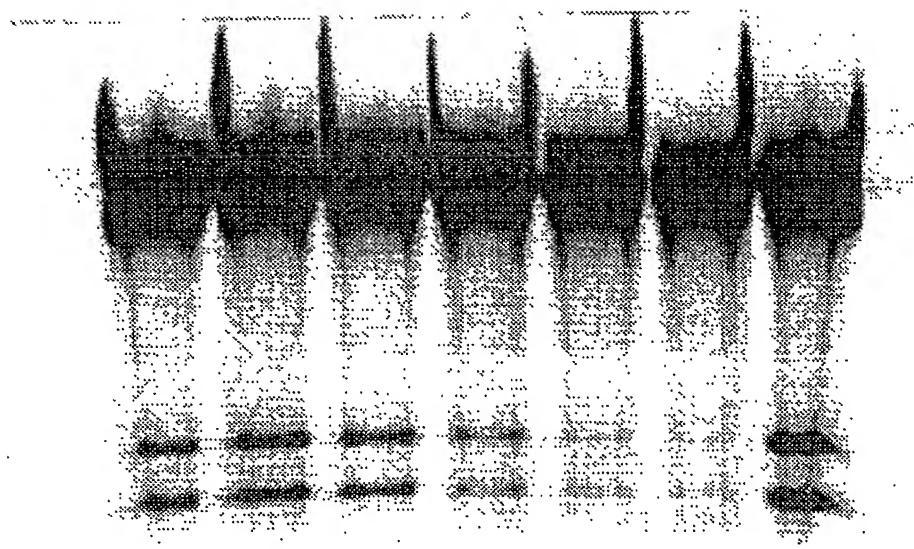


FIG. 51

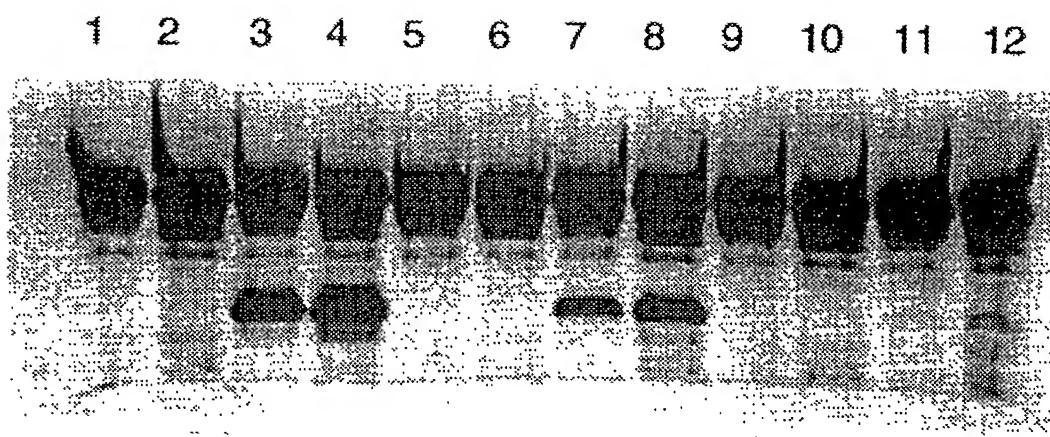


FIG. 52

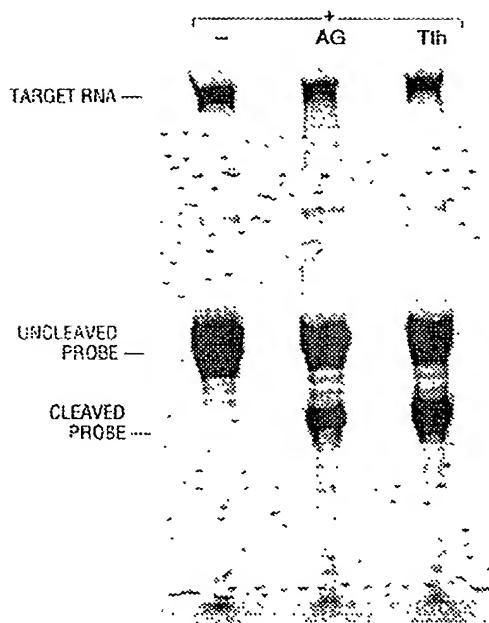


FIG. 53A

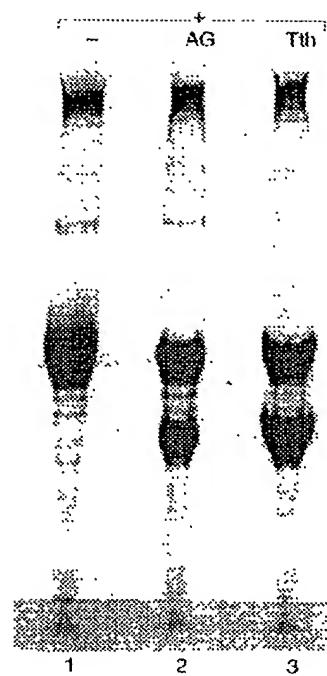


FIG. 53B

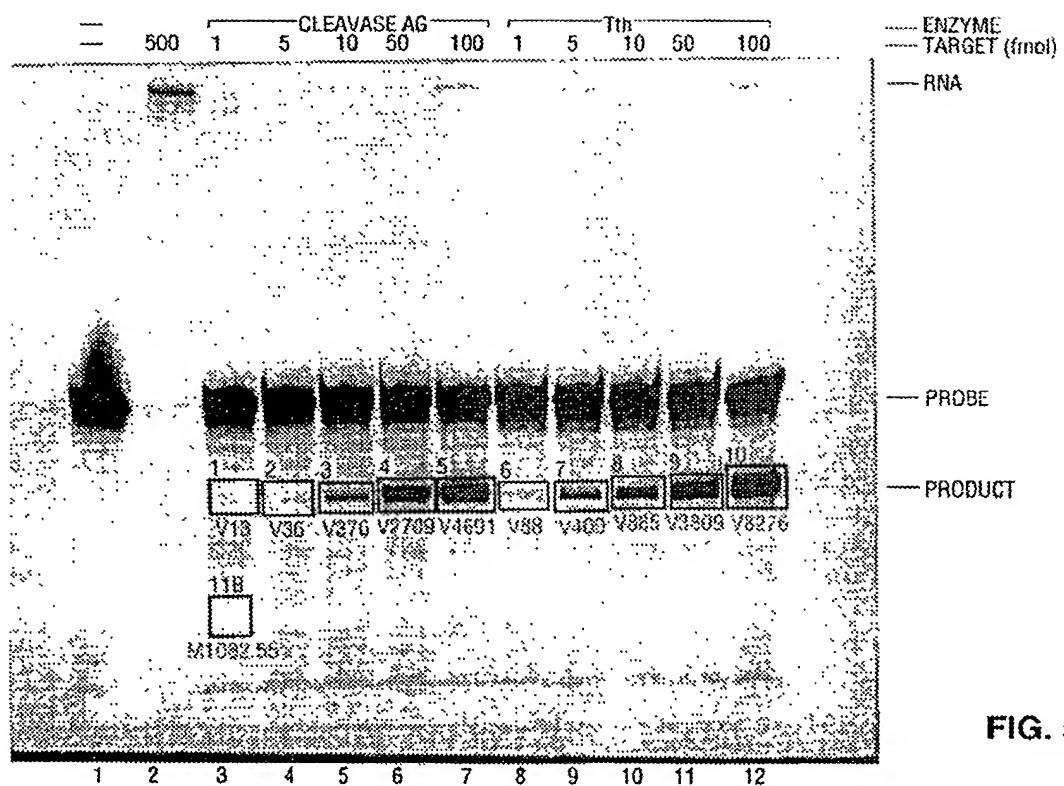


FIG. 54

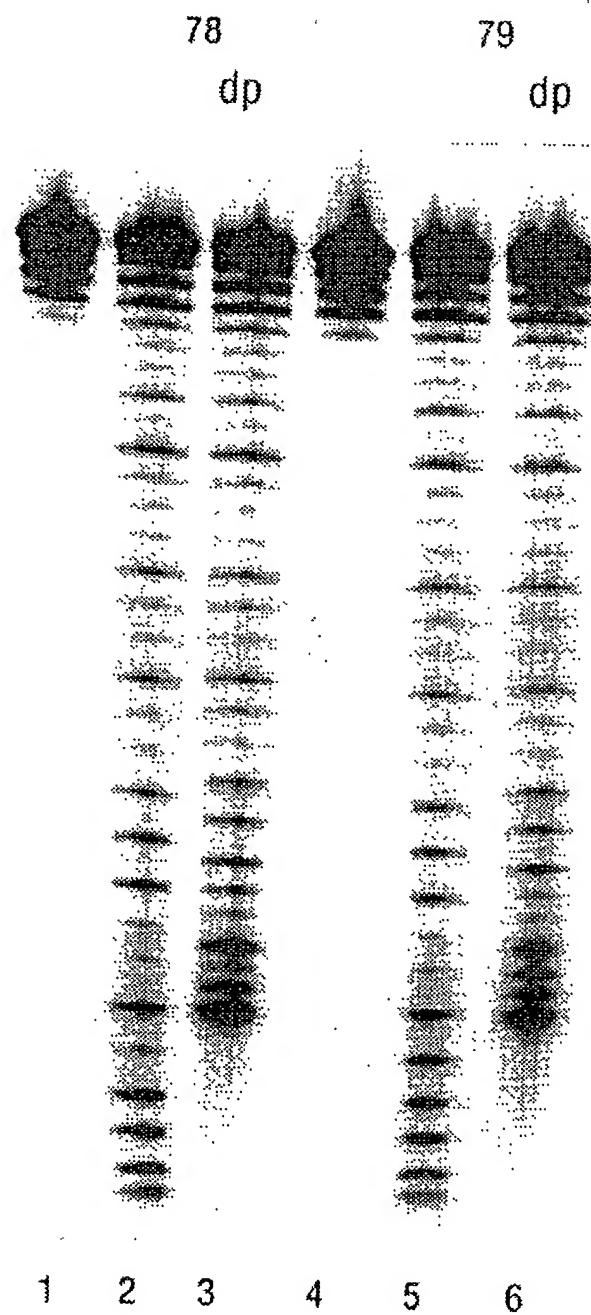


FIG. 55

70 (C10 amino T's)
74 (C6 amino T's)

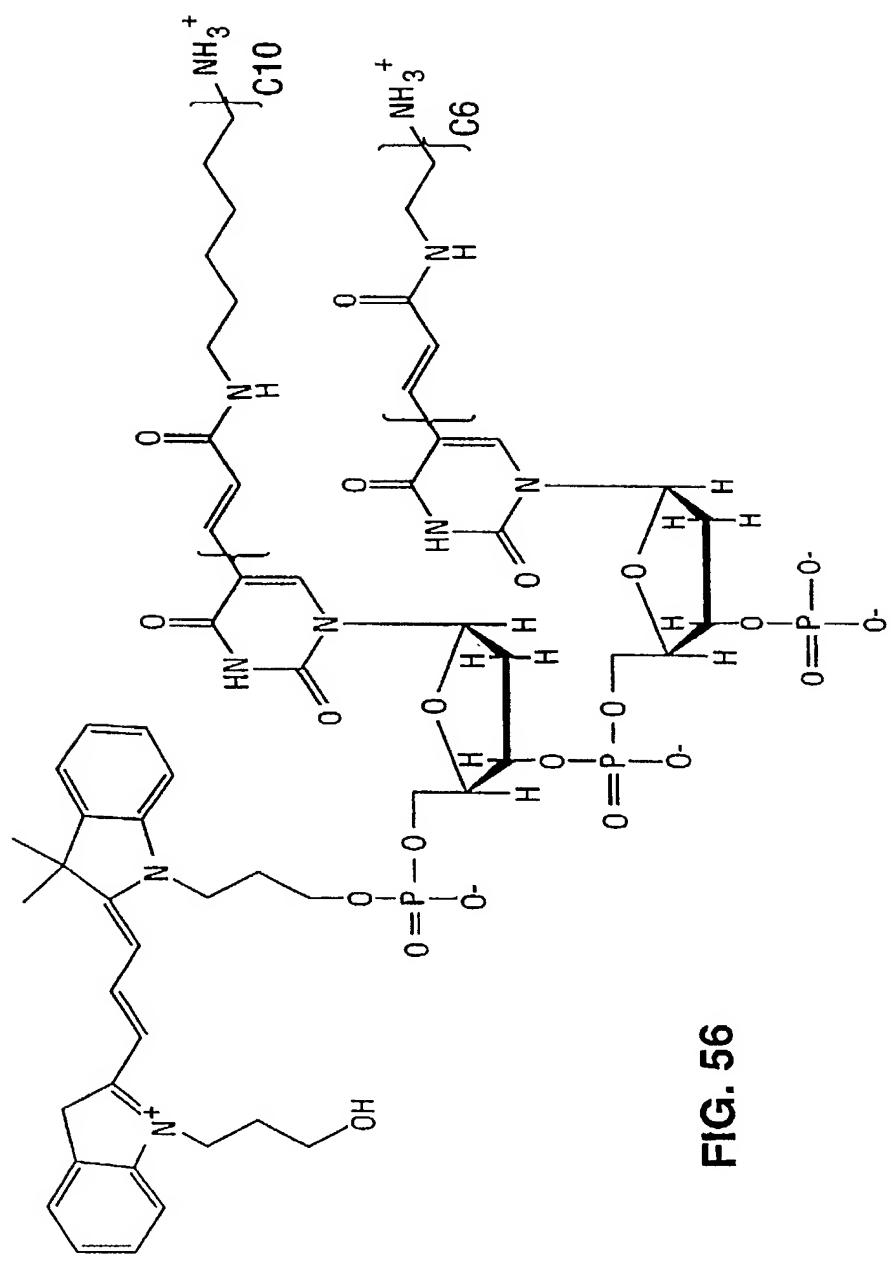
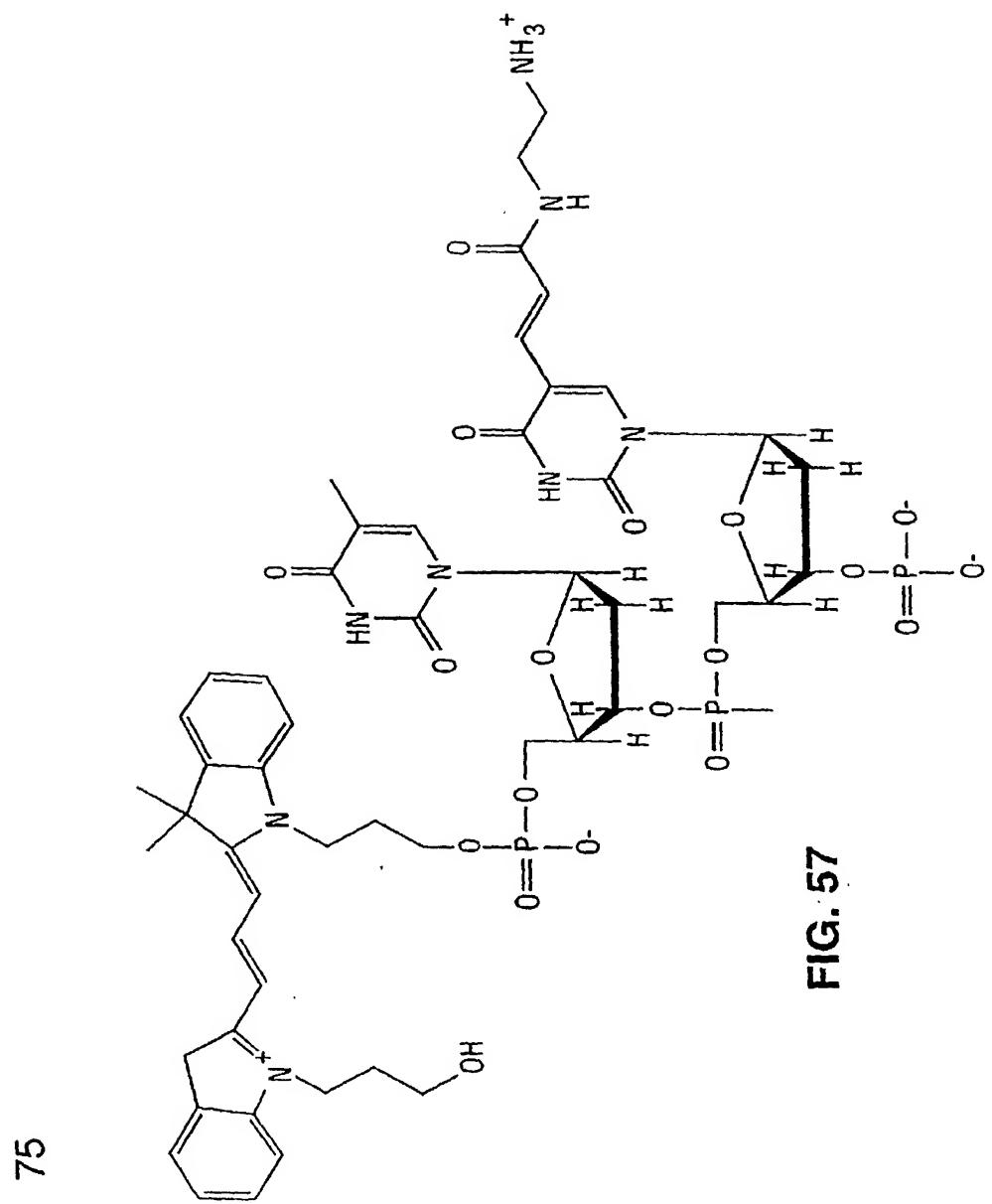


FIG. 56



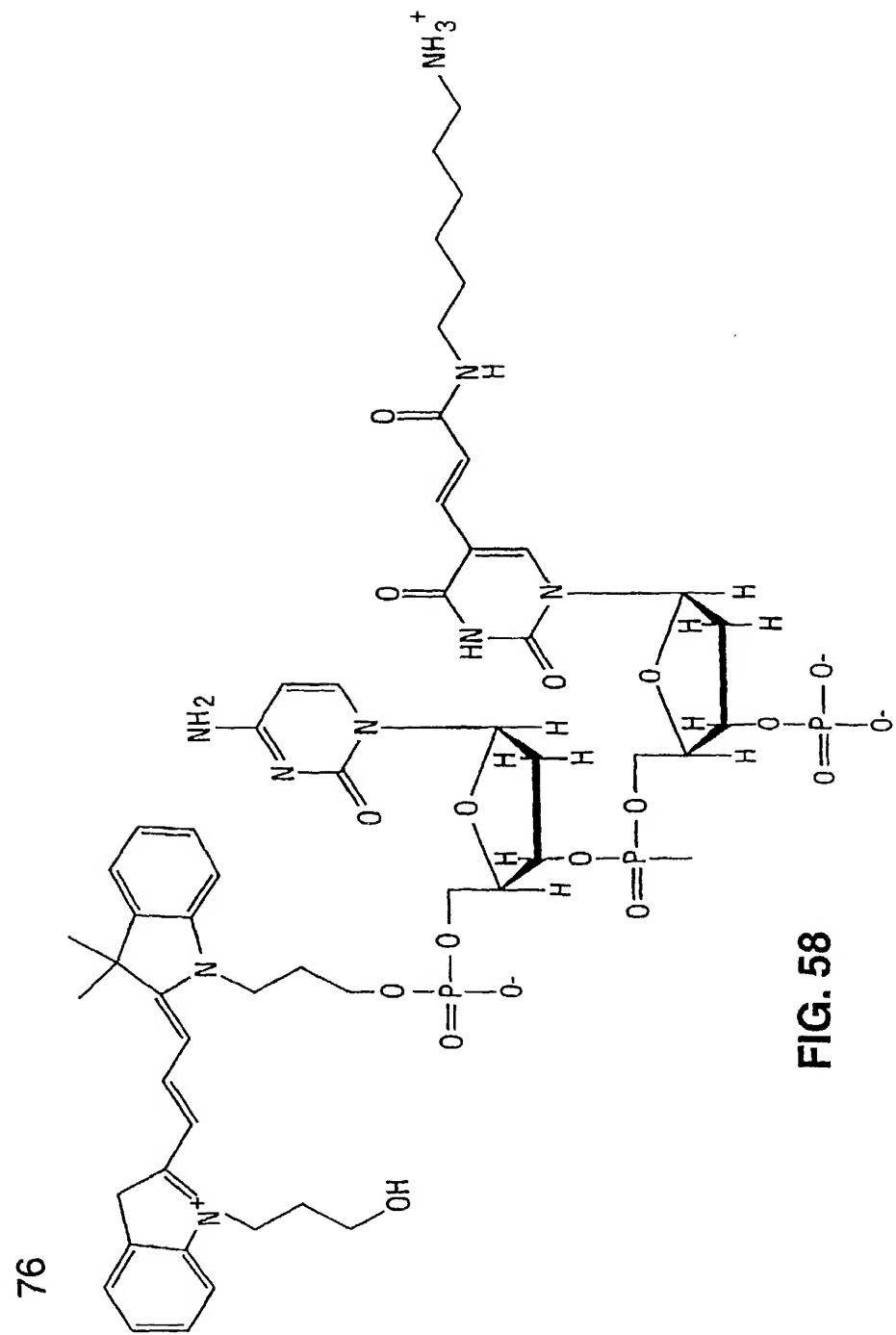


FIG. 58

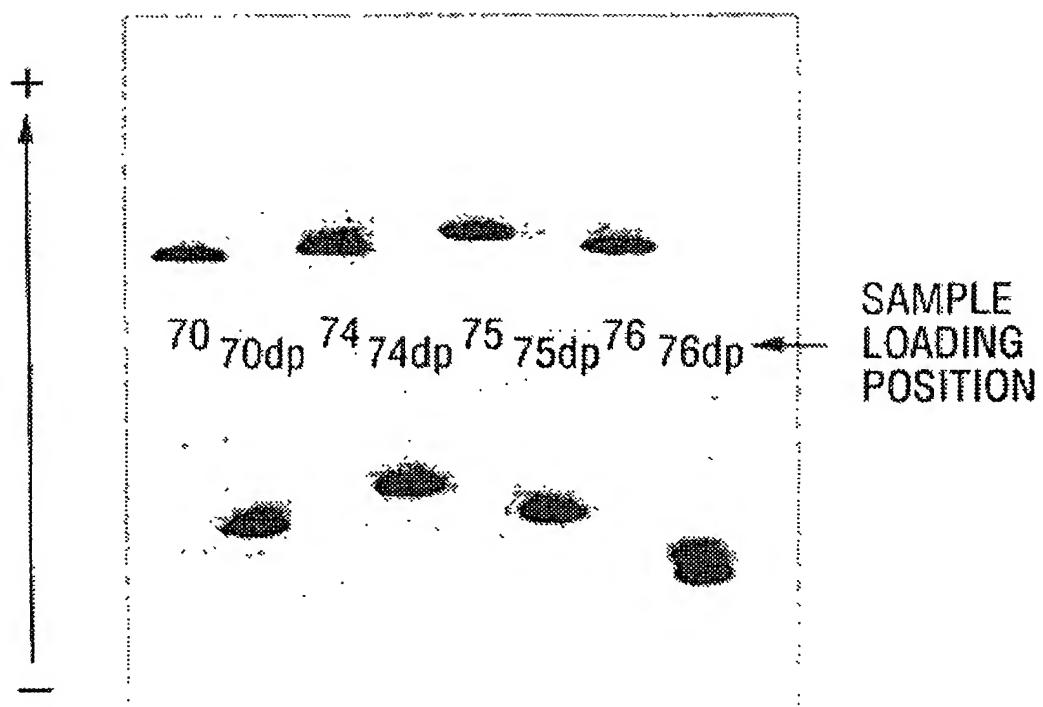


FIG. 59

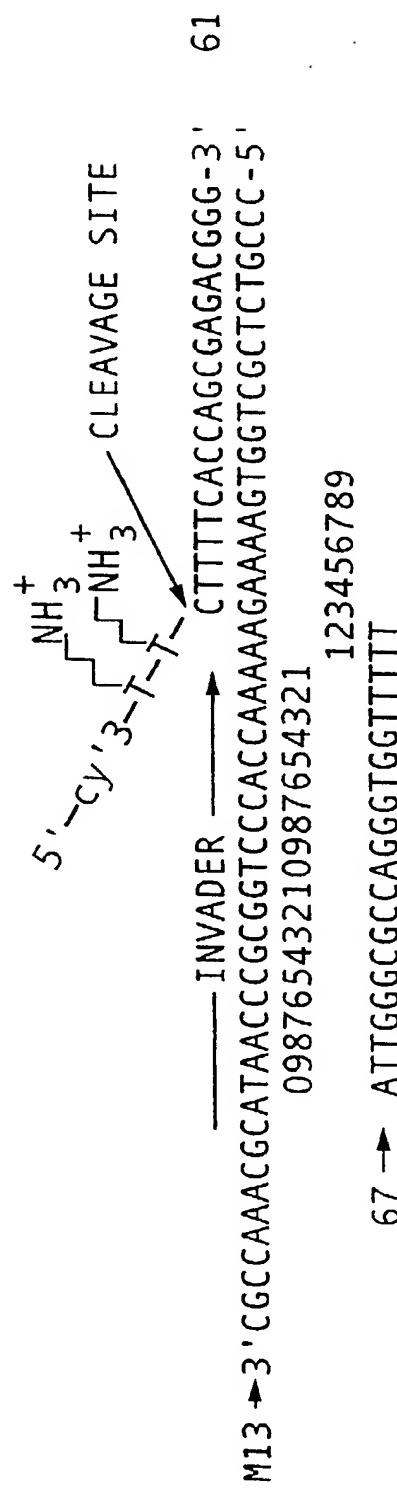


FIG. 60A

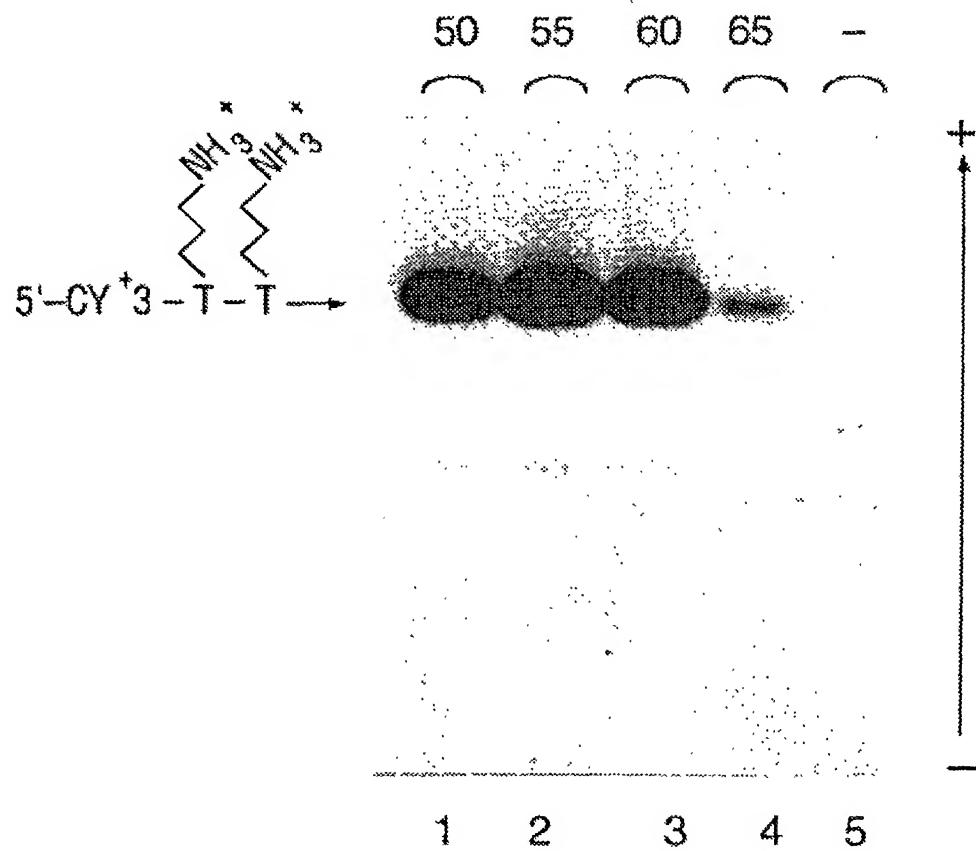


FIG. 60B

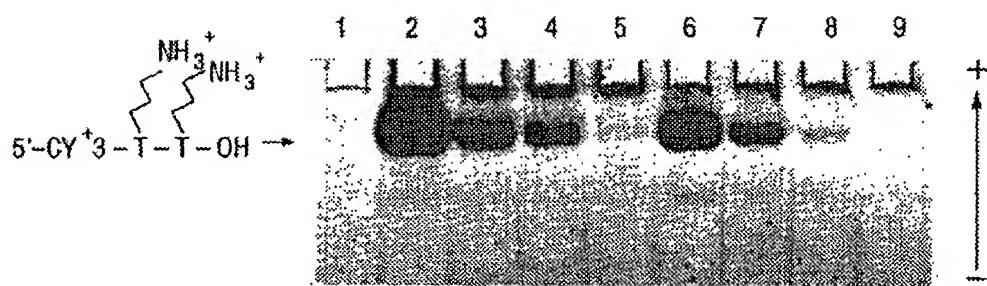


FIG. 61

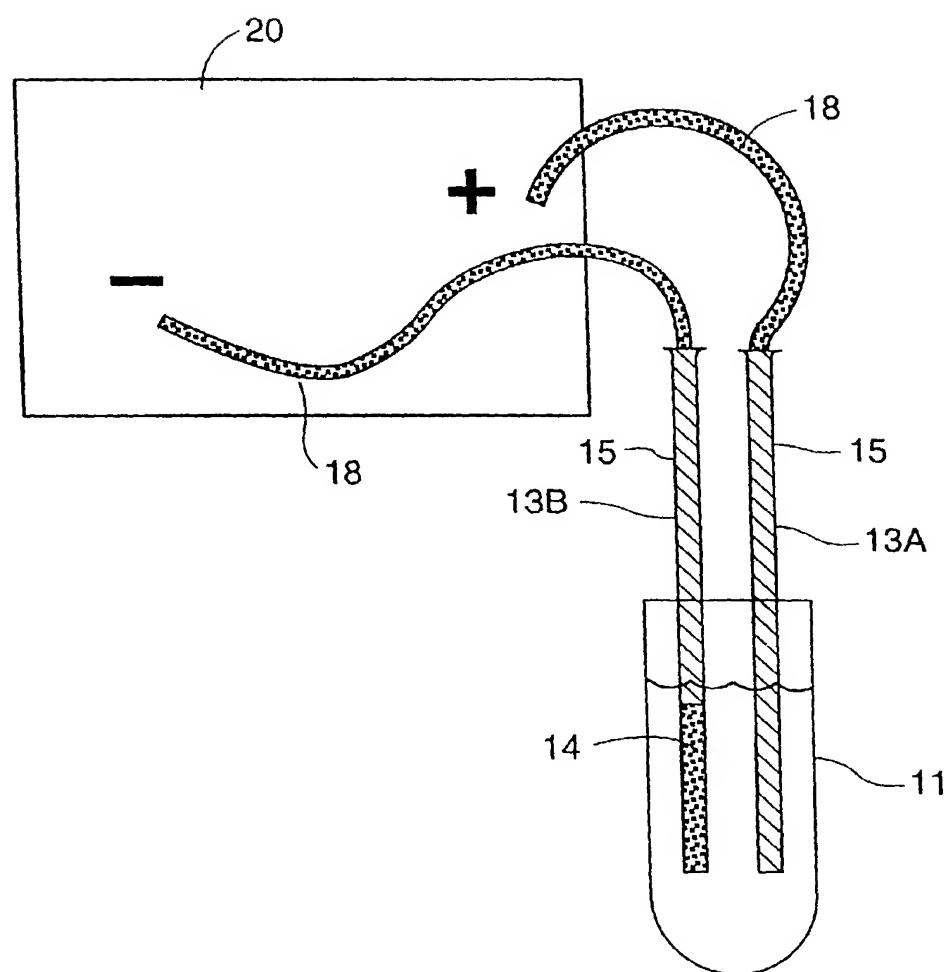


FIG. 62

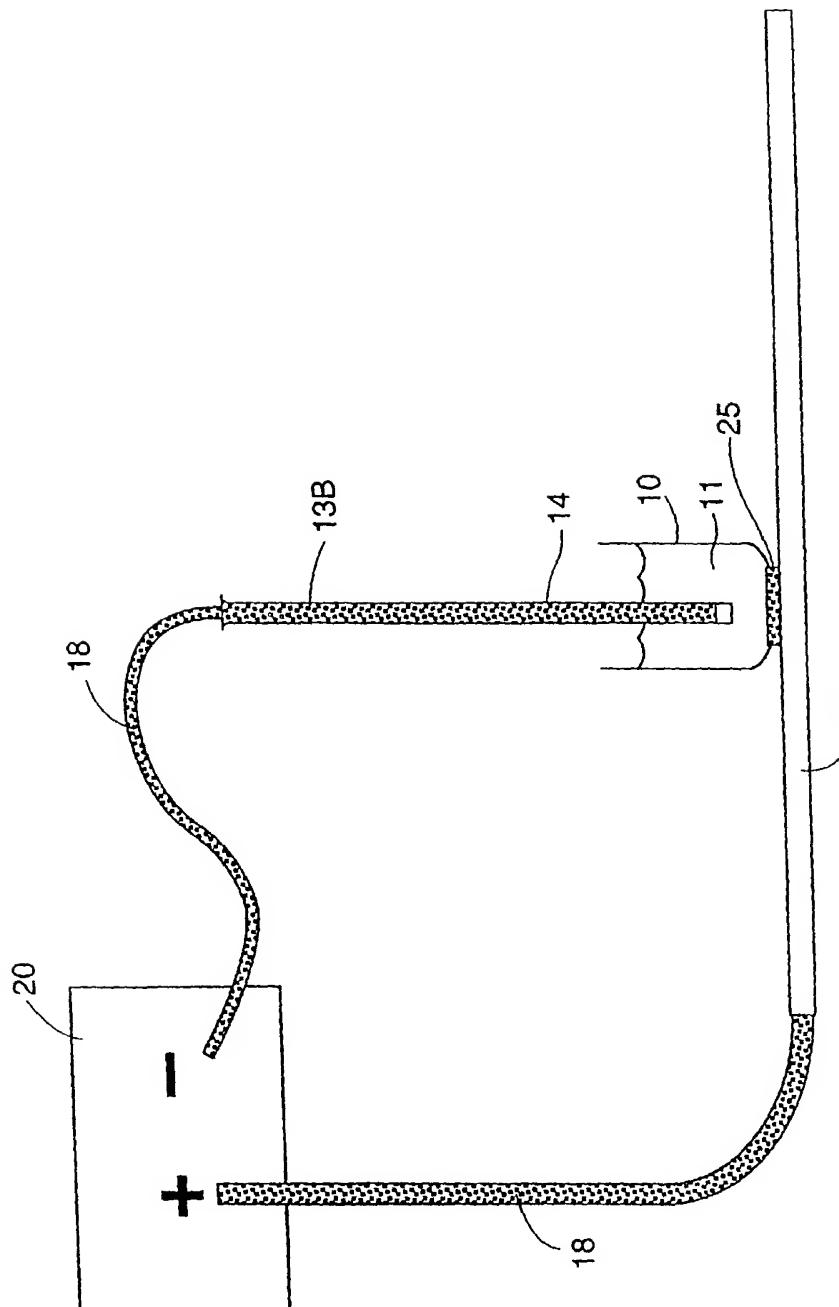


FIG. 63

10074228, 06/1978



FIG. 64



FIG. 65A

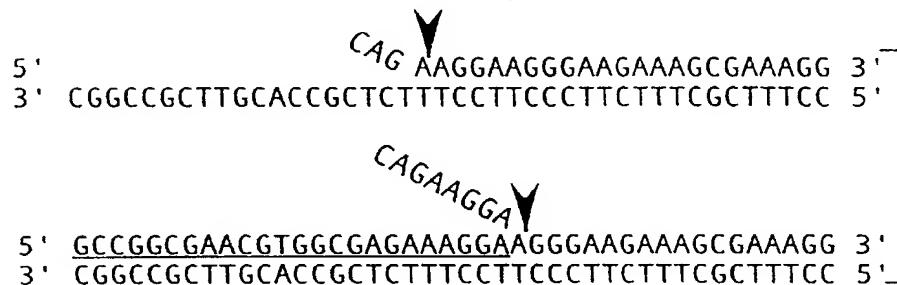


FIG. 65B



FIG. 65C

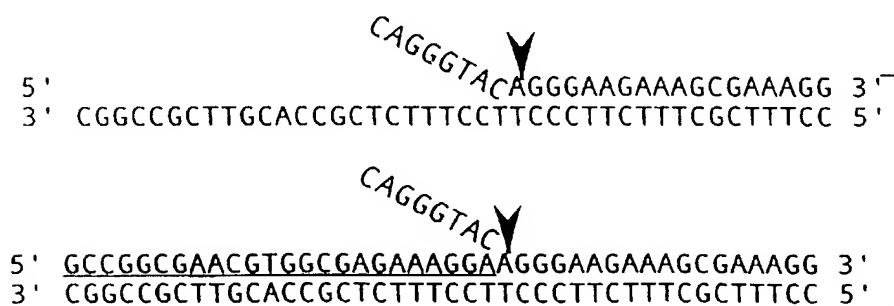


FIG. 65D

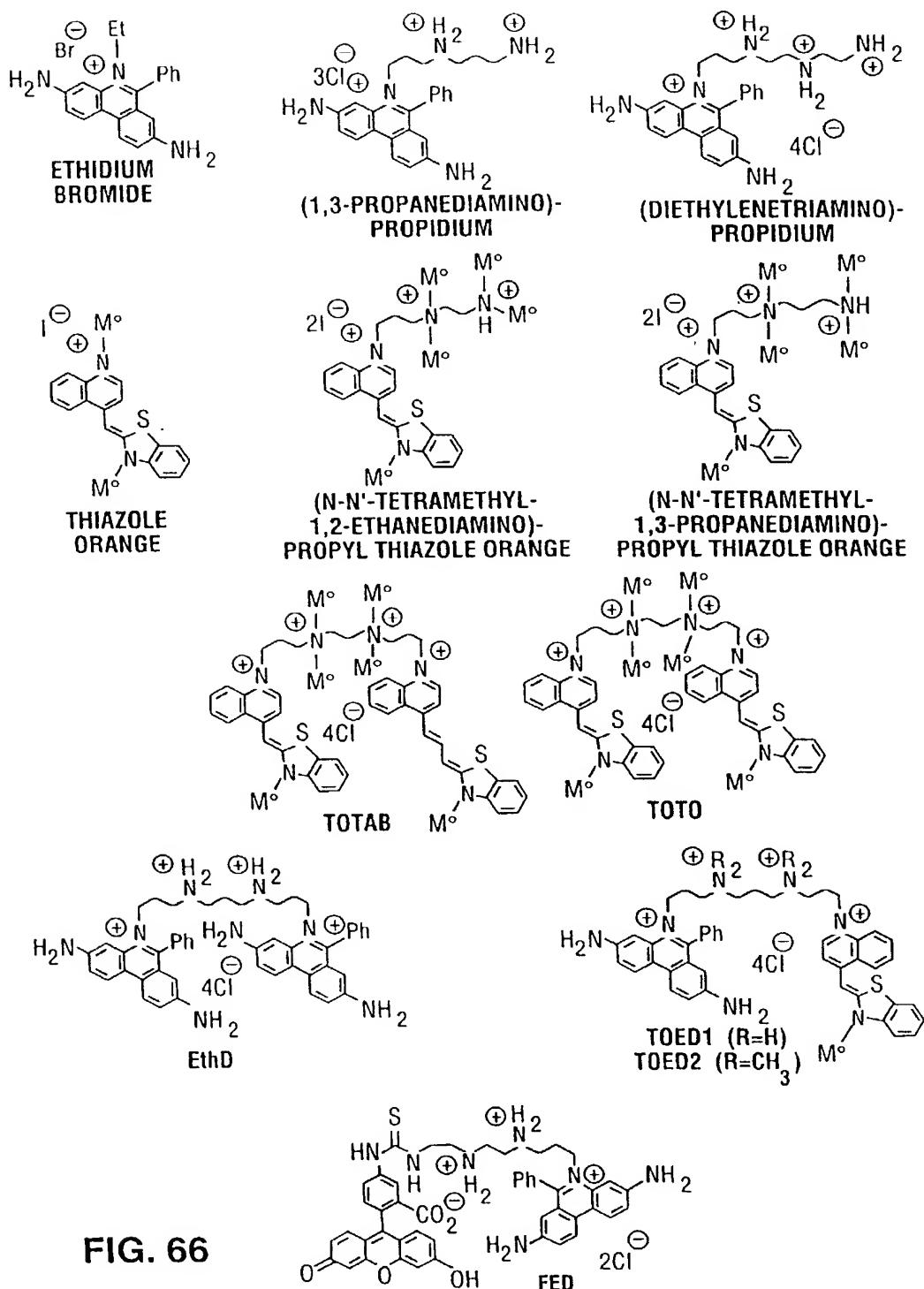


FIG. 66